

O'Bryen, Barbara

From: Hale, Mary
Sent: Tuesday, May 10, 2005 9:40 AM
To: Wacławiw, Alexandra; O'Bryen, Barbara; Shears, Beverly; Schreiber, David; Arnold, Deirdre; Hart, Edward; Delaval, Jan; Ruhl, Mary Jane; Jarrell, Noble; Schulwitz, Paul; Sheppard, Paula; Port, Toby
Subject: FW: sequence search

If you have this search please let me know and contact Bridget with the status.

Thanks,
Mary

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Tuesday, May 10, 2005 9:36 AM
To: Hale, Mary
Subject: FW: sequence search

Mary Ms. Bunner inquired about this search, it has been logged in but not completed.

-----Original Message-----

From: Bunner, Bridget
Sent: Wednesday, April 27, 2005 4:12 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/892,360 (please include the pending databases):

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

*Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70*

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 28, 2005, 13:22:27 ; Search time 43 Seconds
(without alignments)
933.981 Million cell updates/sec

Title: US-09-892-360-2

Perfect score: 2760

Sequence: 1 MFPLYTDFLSLVAVPAAAP.....IPTDTKREPNNSLLEDRN 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2.6/ptodata/1/1aa/5A-COMB.pep:*

2: /cgn2.6/ptodata/1/1aa/5B-COMB.pep:*

3: /cgn2.6/ptodata/1/1aa/6A-COMB.pep:*

4: /cgn2.6/ptodata/1/1aa/6B-COMB.pep:*

5: /cgn2.6/ptodata/1/1aa/PCTUS-COMB.pep:*

6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2760	100.0	538	4	US-09-949-016-7001
2	2760	100.0	538	4	US-09-949-016-7368
3	1248.5	45.2	411	3	US-09-236-080-6
4	1242.5	45.0	411	3	US-09-236-080-2
5	1242.5	45.0	411	3	US-09-336-643A-83
6	1238.5	44.9	370	3	US-09-144-914-8
7	822.5	29.8	419	4	US-09-949-016-6913
8	822.5	29.8	440	4	US-09-949-016-7809
9	812.5	29.4	393	4	US-09-432-470-2
10	812.5	29.4	393	4	US-09-432-470-2
11	483	17.5	499	4	US-09-561-763-2
12	483	17.5	499	4	US-09-431-367B-2
13	447	16.2	107	3	US-09-236-080-4
14	403	14.6	336	3	US-08-749-816-2
15	403	14.6	336	3	US-09-144-914-2
16	396	14.3	332	4	US-09-561-763-5
17	396	14.3	332	4	US-09-431-367B-5
18	361	13.1	361	4	US-09-362-842-14
19	352.5	12.8	405	3	US-09-144-914-5
20	349.5	12.7	394	3	US-09-144-914-4
21	342	12.4	388	4	US-09-949-016-7631
22	333.5	12.1	313	3	US-09-336-643A-81
23	333.5	12.1	313	4	US-09-561-763-8
24	333.5	12.1	313	4	US-09-431-367B-8
25	323	11.7	408	4	US-09-362-842-12
26	295.5	10.7	273	4	US-09-949-016-7794
27	290.5	10.5	618	1	US-08-332-312-2

28	287	10.4	257	4	US-09-949-016-6654	Sequence 6654, Ap
29	233.5	8.5	995	4	US-09-362-842-2	Sequence 2, Appli
30	233	8.4	395	4	US-09-362-842-6	Sequence 6, Appli
31	220	8.0	401	4	US-09-561-763-11	Sequence 11, Appli
32	220	8.0	401	4	US-09-431-367B-11	Sequence 11, Appli
33	212.5	7.7	336	1	US-08-332-312-4	Sequence 4, Appli
34	197	7.1	730	4	US-09-362-842-4	Sequence 4, Appli
35	197	7.1	741	4	US-09-362-842-67	Sequence 67, Appli
36	197	7.1	741	4	US-09-270-767-45442	Sequence 45442, A
37	186.5	6.8	1153	4	US-09-362-842-8	Sequence 8, Appli
38	164.5	6.0	347	3	US-08-749-816-3	Sequence 3, Appli
39	164.5	6.0	347	3	US-09-144-914-6	Sequence 6, Appli
40	162	5.9	308	4	US-09-248-796A-20134	Sequence 20134, A
41	159	5.8	383	3	US-08-749-816-4	Sequence 4, Appli
42	159	5.8	383	3	US-09-144-914-7	Sequence 7, Appli
43	137.5	5.0	146	4	US-09-362-842-69	Sequence 69, Appli
44	137.5	5.0	146	4	US-09-270-767-31685	Sequence 31685, A
45	134	4.9	197	3	US-09-336-643A-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-7001
; Sequence 7001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7001
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7001

Query Match	100.0%	Score 2760;	DB 4;	Length 538;
Best Local Similarity	100.0%	Pred. No. 1.3e-246;	Mismatches 0;	Indels 0; Gaps 0;
Matches 538;	Conservative 0;			
QY	1	MFPLYTDFLSLVAVPAAAPVCQPKSATNGQPPAPPTPTPLRSISSRATVVARMEGTSQ	60	
DB	1	MFPLYTDFLSLVAVPAAAPVCQPKSATNGQPPAPPTPTPLRSISSRATVVARMEGTSQ	60	
QY	61	GGLOTVMKTKTVAIFVWVYVLTGVLFPALQPPSSOKNTIALEKAEFLRDHVCVS	120	
DB	61	GGLOTVMKTKTVAIFVWVYVLTGVLFPALQPPSSOKNTIALEKAEFLRDHVCVS	120	
QY	121	POELETIIQHALDADNAGVSPIGNSNNSHWDLSGSAFFAGTGTITTYGNIAPSTEGG	180	
DB	121	POELETIIQHALDADNAGVSPIGNSNNSHWDLSGSAFFAGTGTITTYGNIAPSTEGG	180	
QY	181	KIFCILYAFIGPLFGFLLAGIGDQGTIFGKSIAARVEKVPFRKKQVSQTKIRVISTILFI	240	
DB	181	KIFCILYAFIGPLFGFLLAGIGDQGTIFGKSIAARVEKVPFRKKQVSQTKIRVISTILFI	240	
QY	241	LACGICVFVTIPAVIFKYEIEGHTALESIFVWVYVLTGVLFPALQPPSSOKNTIALEKAEFLRDHVCVS	300	
DB	241	LACGICVFVTIPAVIFKYEIEGHTALESIFVWVYVLTGVLFPALQPPSSOKNTIALEKAEFLRDHVCVS	300	
QY	301	WFVILVGLYPAAVLSMIGDMLRVLSKTKKEVGEIKAHAAAEWKNVTAEPRETRRLSV	360	

Db 301 WFWILVGLYFAAVLSMIGDWRVLSKTKTEVEGEIKAHAAEWKANTAEFRTRRLSV 360
Qy 361 EIHDKLQRAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTCGRFKASSOESINNR 420
Db 361 EIHDKLQRAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTCGRFKASSOESINNR 420
Qy 421 NNRLKGPQLNKHGQGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
Db 421 NNRLKGPQLNKHGQGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
Qy 481 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLEDNR 538
Db 481 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLEDNR 538
RESULT 2
US-09-949-016-7368
; Sequence 7368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7368
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7368

Query Match 100.0%; Score 2760; DB 4; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.4e-246;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPFLYTDFFLSLVAPAAAPVCPKATNGQPPAPPTPTPLSLSSRATVVAARMGTSQ 60
Db 21 MPFLYTDFFLSLVAPAAAPVCPKATNGQPPAPPTPTPLSLSSRATVVAARMGTSQ 80
Qy 61 GGLQTVMKWKTVAIFVWVVLVTGGLVFRALDQPFSSQKNTIALEKAEFLRDHVCVS 120
Db 81 GGLQTVMKWKTVAIFVWVVLVTGGLVFRALDQPFSSQKNTIALEKAEFLRDHVCVS 140
Qy 121 POELETLIQHALDADNAGVSPIGNSSNSHWDLGSAFFAGTVITIGVNIAPSTEGG 180
Db 141 POELETLIQHALDADNAGVSPIGNSSNSHWDLGSAFFAGTVITIGVNIAPSTEGG 200
Qy 181 KIFCILYALFGIFLGLAGIGDQGTIFGKSIARVEKVKQVSOTKIRVISTILFI 240
Db 201 KIFCILYALFGIFLGLAGIGDQGTIFGKSIARVEKVKQVSOTKIRVISTILFI 260
Qy 241 LAGCIVFTVPIVIFKYGWTALESIFVWVVLVTGFGDFVAGGNAGINREWKPLV 300
Db 261 LAGCIVFTVPIVIFKYGWTALESIFVWVVLVTGFGDFVAGGNAGINREWKPLV 320
Qy 301 WFWILVGLYFAAVLSMIGDWRVLSKTKTEVEGEIKAHAAEWKANTAEFRTRRLSV 360
Db 321 WFWILVGLYFAAVLSMIGDWRVLSKTKTEVEGEIKAHAAEWKANTAEFRTRRLSV 380
Qy 361 EIHDKLQRAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTCGRFKASSOESINNR 420
Db 381 EIHDKLQRAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTCGRFKASSOESINNR 440

Qy 421 NNRLKGPQLNKHGQGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 480
Db 441 NNRLKGPQLNKHGQGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNY 500
Qy 481 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLEDNR 538
Db 501 LDEEKEBEETKCKNSDNSSTAMLTDCIOQHAELENGMIPTDTKOREPENNSLLEDNR 558
RESULT 3
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6
Query Match 45.2%; Score 1248.5; DB 3; Length 411;
Best Local Similarity 64.3%; Pred. No. 7e-107;
Matches 247; Conservative 53; Mismatches 67; Indels 17; Gaps 5;
Qy 17 AAAPVCPKATNGQPPAPPTPTPLSLSSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
Db 2 AAPDLDPKSA-----AQNSKPLRSFSKPTVLASRVSDS---AINVMKWKTVSTI 50
Qy 76 FVWVVLVTGGLVFRALDQPFSSQKNTIALEKAEFLRDHVCVSPOELETLIQHALDAD 135
Db 51 FLVWVLYLIGAAVFAKLEQPOEISORTIVIQKTFIAQHACVNSTELDELIIQIVAAI 110
Qy 136 NAGVSPIGNSSNSHWDLGSAFFAGTVITIGVNIAPSTEGGKIFCILYALFGIFL 195
Db 111 NAGIIPLGNSNQVSHWDLGSSFFAGTVITIGVNIAPSTEGGKIFCILYALFGIFL 170
Qy 196 GFLLAGIGDQGTIFGKSIARVEKVKQVSOTKIRVISTILFIAGCIVFTVPIV 255
Db 171 GFLLAGIGDQGTIFGKSIARVEKVKQVSOTKIRVISTILFIAGCIVFTVPIV 230
Qy 256 KYIEGWTALLESIFVWVVLVTGFGDFVAGGNAGINREWKPLVWVWVWVWVWVWV 315
Db 231 KHIEGWSALDAIYFVWVITLTIGFGDVVAGG-SDIEYLDYFKPVVWVWVWVWV 289
Qy 316 SMIGDLRVLSKTKTEVEGEIKAHAAEWKANTAEFRTRRLSVIHDKLOAAATIRSM 375
Db 290 SMIGDLRVLSKTKTEVEGEIKAHAAEWKANTAEFRTRRLSVIHDKLOAAATIRSM 346
Qy 376 BRRRLGLQORAHSLDMLSPKRSV 399
Db 347 -KRKLSAELAGNHNOELTPCMRTL 369
RESULT 4
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

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SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-080-2

Query Match
Best Local Similarity 45.0%; Score 1242.5; DB 3; Length 411;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCQPKSATNGOPAPAPTPTPRLSISSRATVVA-RMEGTSQGLQTVNMKKTVAI 75
Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTVSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSOKNTIALEKAEFLRDHVCVSPQELTIIQHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAI 110

QY 136 NAGVSPIGNSSNNSHWDLSGSAFFPAGTIVTTIGYGNIAFSTEGGKIFCIIYAFGPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTIGFNGNISPRTEGGKIFCIIYALLGPIPLF 170

QY 196 GFLLAGIGDQGTIFGKSIARVEKVKFRKQVSTQKIRVISTITLFIILAGCIVFVTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKGIKAVEDTFIKWNVSTQKIRIISTITFIILFGCVLFAVLPALIF 230

QY 256 KIEGHTALESIVFVVVLTITTVGFGDPVAGGNAGINREWKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGHSALDAIYFVVVLTITTVGFGDYVAGG-SDIEYLDYFKPVVWFWILVGLAYFAAVL 289

QY 316 SMIGDWLRVLSKTKKEEVEGIEKAHAAEWKANVTAEFRETERRLSVEIHDKLOPAAATIRSM 375
Db 290 SMIGDWLRVLSKTKKEEVEGFRAHAAEWNTANVTAEPKETERRLSVIYDKFQRTSI--- 346

QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
Db 347 -KKLSAELAGNHQELTFCRRTL 369
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RESULT 5

```
US-09-336-643A-83
Sequence 83, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 411
TYPE: PRT
ORGANISM: H. sapiens
US-09-336-643A-83
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Query Match
Best Local Similarity 45.0%; Score 1242.5; DB 3; Length 411;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCQPKSATNGOPAPAPTPTPRLSISSRATVVA-RMEGTSQGLQTVNMKKTVAI 75
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Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKKTVSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSOKNTIALEKAEFLRDHVCVSPQELTIIQHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAI 110

QY 136 NAGVSPIGNSSNNSHWDLSGSAFFPAGTIVTTIGYGNIAFSTEGGKIFCIIYAFGPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTIGFNGNISPRTEGGKIFCIIYALLGPIPLF 170

QY 196 GFLLAGIGDQGTIFGKSIARVEKVKFRKQVSTQKIRVISTITLFIILAGCIVFVTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKGIKAVEDTFIKWNVSTQKIRIISTITFIILFGCVLFAVLPALIF 230

QY 256 KIEGHTALESIVFVVVLTITTVGFGDPVAGGNAGINREWKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGHSALDAIYFVVVLTITTVGFGDYVAGG-SDIEYLDYFKPVVWFWILVGLAYFAAVL 289

QY 316 SMIGDWLRVLSKTKKEEVEGIEKAHAAEWKANVTAEFRETERRLSVEIHDKLOPAAATIRSM 375
Db 290 SMIGDWLRVLSKTKKEEVEGFRAHAAEWNTANVTAEPKETERRLSVIYDKFQRTSI--- 346

QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
Db 347 -KKLSAELAGNHQELTFCRRTL 369

RESULT 6
US-09-144-914-8
Sequence 8, Application US/09144914
Patent No. 6309855
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: TREK-1
US-09-144-914-8

Query Match
Best Local Similarity 44.9%; Score 1238.5; DB 3; Length 370;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;

QY 17 AAAPVCQPKSATNGOPAPAPTPTPRLSISSRATVVA-RMEGTSQGLQTVNMKKTVAI 75
Db 2 AAPDLLDPKSA-----AONSKPRLSPSTKPTVLASRVESDS---AINVMKKTVSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSOKNTIALEKAEFLRDHVCVSPQELTIIQHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110

QY 136 NAGVSPIGNSSNNSHWDLSGSAFFPAGTIVTTIGYGNIAFSTEGGKIFCIIYAFGPIPLF 195
Db 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTIGFNGNISPRTEGGKIFCIIYALLGPIPLF 170
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QY 196 GFLLAGIGDGLTIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFTIPAVIF 255
 Db 171 GFLLAGVGDLGTFGKGIKAVEDTFIKNVSTQKIRIISTIFILFGCVLFAVAFVIF 230
 QY 256 KYIEGWTALIESIYFVVVTLTTVGDFGVAGNAGINREWKPLVFWFVLGLAYFAAVL 315
 Db 231 KHIEGWSALDAIYFVITLTTIGFDYVAGG-SDIEYLFYKVEVWFWFVLGLAYFAAVL 289
 QY 316 SMIGDMLRVLSKTKKEVEGVIKAAHAEWKANVTAEFRETRRLSVEIHDKLOAAITRSM 375
 Db 290 SMIGDMLRVLSKTKKEVEGFRAHAEWTANVTAEFKTRRLSVELYDFKQRTSV--- 346
 QY 376 ERRRLGLDQRAHSLDMLSPKRS 398
 Db 347 -KEKLSAELAGNHQELTPCMT 368

RESULT 7

US-09-949-016-6913
 ; Sequence 6913, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6913
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-6913

Query Match 29.8%; Score 822.5; DB 4; Length 419;
 Best Local Similarity 48.4%; Pred. No. 2e-67;
 Matches 164; Conservative 55; Mismatches 87; Indels 33; Gaps 4;
 QY 20 PVCQPKSATNGQPPAPPTPTPLSLSSRATVVARMEGTSQGLQTVMKKTVAIFVVV 79
 Db 8 PPARPLQAGSGAGPAG-----RAMRSTTLLALLV 39
 QY 80 VVYLVTVGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDADNAGV 139
 Db 40 LLLVLSGALVFRALQEPHEQQAQRELGEVREKFLRAHPCVSDQELGLLKEVADALGGGA 99
 QY 140 SPFGNSNNSSH--WDLGSAFFAGTVITIGYNTIAPSTEGGKIFCILYAIPIGIFLPGF 197
 Db 100 DPETNSTNSHSAWDLGSAFFSGTITITIGYGNVALRTDAGRLFCIFYALVGIPLFI 159
 QY 198 LLAGIGDGLTIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFTIPAVIFKY 257
 Db 160 LLAGVGDRGLSSLRHGIGHIEAIFLKHVPPPELVRLSAMLFLICLLFVLTPFTVFCY 219
 QY 258 IEQWTALIESIYFVVVTLTTVGDFGVAGNAGINREWKPLVFWFVLGLAYFAAVL 317
 Db 220 MEDWSKLEAIYFVITLTTVGFDYVAGADPRQD-SPAYQPLVFWFVLGLAYFASVLT 278
 QY 318 IGDWLRVLSKTKKEVEGEIKAAHAEWKANVTAEFRETR 356
 Db 279 IGNWLRVSRTRAEAGGLTAQAASWTGTVA--RVTOR 315

RESULT 8

US-09-949-016-7809
 ; Sequence 7809, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7809
 ; LENGTH: 440
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-7809

Query Match 29.8%; Score 822.5; DB 4; Length 440;
 Best Local Similarity 48.4%; Pred. No. 2.1e-67;
 Matches 164; Conservative 55; Mismatches 87; Indels 33; Gaps 4;
 QY 20 PVCQPKSATNGQPPAPPTPTPLSLSSRATVVARMEGTSQGLQTVMKKTVAIFVVV 79
 Db 29 PPARPLQAGSGAGPAG-----RAMRSTTLLALLV 60
 QY 80 VVYLVTVGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDADNAGV 139
 Db 61 LLLVLSGALVFRALQEPHEQQAQRELGEVREKFLRAHPCVSDQELGLLKEVADALGGGA 120
 QY 140 SPFGNSNNSSH--WDLGSAFFAGTVITIGYNTIAPSTEGGKIFCILYAIPIGIFLPGF 197
 Db 121 DPETNSTNSHSAWDLGSAFFSGTITITIGYGNVALRTDAGRLFCIFYALVGIPLFI 180
 QY 198 LLAGIGDGLTIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFTIPAVIFKY 257
 Db 181 LLAGVGDRGLSSLRHGIGHIEAIFLKHVPPPELVRLSAMLFLICLLFVLTPFTVFCY 240
 QY 258 IEQWTALIESIYFVVVTLTTVGDFGVAGNAGINREWKPLVFWFVLGLAYFAAVL 317
 Db 241 MEDWSKLEAIYFVITLTTVGFDYVAGADPRQD-SPAYQPLVFWFVLGLAYFASVLT 299
 QY 318 IGDWLRVLSKTKKEVEGEIKAAHAEWKANVTAEFRETR 356
 Db 300 IGNWLRVSRTRAEAGGLTAQAASWTGTVA--RVTOR 336

RESULT 9

US-09-432-470-2
 ; Sequence 2, Application US/09432470
 ; Patent No. 6426197
 ; GENERAL INFORMATION:
 ; APPLICANT: David Malcolm Duckworth
 ; APPLICANT: Conrad Gerald Chapman
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30190
 ; CURRENT APPLICATION NUMBER: US/09/432,470
 ; PRIOR FILING DATE: 1999-11-03
 ; EARLIER APPLICATION NUMBER: UK 9923668.9
 ; EARLIER FILING DATE: 1999-10-07
 ; EARLIER APPLICATION NUMBER: UK 9824048.4
 ; EARLIER FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 393
 ; TYPE: PRT

ORGANISM: HOMO SAPIENS
US-09-432-470-2

Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;

QY 67 MKWTKVVAIFVVVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 126
DB 1 MRSTLLALLLVLLVNSGALVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 60
QY 127 LIQHALDADNAGVSPGNSNNSH--WDLGSAFFPAGTVITIGVNIAPSTEGKIFC 184
DB 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFPAGTVITIGVNIAPSTEGKIFC 120
QY 185 ILYAIFGLPFLGAGDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 244
DB 121 IFYALVGLPFLGAGDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 180
QY 245 IVFVTIPAVIFKIEGWTALSIYFVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 304
DB 181 LLFVLTPTVFCVCMEDWSKLEAIFVIVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 239
QY 305 LVGLAYFAAFLSMIGDNLVLSKTKVEGEIKAHAAEWKANVTAEFRTRR 356
DB 240 LGLAYFASVLTITGNLWVRVSRTRAEWGLTAAQASWTGTVTA--RVTOR 289

RESULT 10

US-09-432-470-4
Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;
GENERAL INFORMATION:
APPLICANT: David Malcolm Duckworth
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30190
CURRENT APPLICATION NUMBER: US/09/432,470
CURRENT FILING DATE: 1999-11-03
EARLIER APPLICATION NUMBER: UK 9923668.9
EARLIER FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: UK 9824048.4
EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 393
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-432-470-4

QY 67 MKWTKVVAIFVVVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 126
DB 1 MRSTLLALLLVLLVNSGALVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 60
QY 127 LIQHALDADNAGVSPGNSNNSH--WDLGSAFFPAGTVITIGVNIAPSTEGKIFC 184
DB 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFPAGTVITIGVNIAPSTEGKIFC 120
QY 185 ILYAIFGLPFLGAGDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 244
DB 121 IFYALVGLPFLGAGDGLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGC 180
QY 245 IVFVTIPAVIFKIEGWTALSIYFVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 304
DB 181 LLFVLTPTVFCVCMEDWSKLEAIFVIVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELT 239
QY 305 LVGLAYFAAFLSMIGDNLVLSKTKVEGEIKAHAAEWKANVTAEFRTRR 356

DB 240 LGLAYFASVLTITGNLWVRVSRTRAEWGLTAAQASWTGTVTA--RVTOR 289

RESULT 11

US-09-561-763-2
Query Match 17.5%; Score 483; DB 4; Length 499;
Best Local Similarity 25.8%; Pred. No. 6.9e-36;
Matches 131; Conservative 81; Mismatches 185; Indels 110; Gaps 14;
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A.J. et al.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-074CP2
CURRENT APPLICATION NUMBER: US/09/561,763
CURRENT FILING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: 09/431,367
PRIOR FILING DATE: 01-11-1999
PRIOR APPLICATION NUMBER: US 09/259,951
PRIOR FILING DATE: 01-03-1999
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 499
TYPE: PRT
ORGANISM: Homo sapiens
US-09-561-763-2

QY 79 VVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELTILQHALDADNAG 138
DB 12 IIFVLAIGAAIFEVLEBPHWKEAKNYYTQKLHLKBPCLGQEGDKILEVVSAAAGQ 71
QY 139 VSPGNSNNSHMDLGSAPFAGTVITIGVNIAPSTEGKIFCILEYAIIEGILPGLF 198
DB 72 VAITGNQTFN--NWNPNAMIFAAVITIGVNIAPSTEGKIFCILEYAIIEGILPGLF 126
QY 199 LAGIGDQLTGIFGKSIARVEKVKQVSTQKIRVISTILFILAGCIVFVTIPAVIFKYI 258
DB 127 LTWI--SALGKFFGGRKALGQFLTKRGVSLRKAQITCTVIFVWGLVHLVIPPVFWMT 185
QY 259 EGWTALESIIYFVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQELTILQHALDADNAG 318
DB 186 EGWNYIEGLYSPFITISTIGFDFVAGVNPSTANTHALYRYFVELWYLGIA----- 236
QY 319 GDMLEVLSTKTKVEGEIKAHAAEWKANVTAEFRTRRLSVEIHDKLOKRAATIRSMER 378
DB 237 --WLSLF-----VNMKVS-----MFVEVHKAIK-----KRRRR 263
QY 379 RLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSOESINNRPNRLK-----CP 428
DB 264 KESPESSPHSRKALQVKGSTASKOVNIFSLSKKEETYNLQIKGKAMKTSGGGETCP 323
QY 429 -EQLNKHQGG-----ASEDNIINKFGSTSLTKRNKDKLTKLPED 468
DB 324 GPGLGPGCGGLPALPPLVPLVYVYVSKRVPVTLSEVSQTLRSKGVSRSPDEEAVARAPED 383
QY 469 VQKIYKTRNYSLEDEKKEE-----TEKWCSDNSSTAMLTDC 507
DB 384 SSPAPEVPMN--OLDRISEECBPWDAQDVHPLIPQDASITFVNTAEGLSDEETSKSLEDN 442
QY 508 I-----QQHAE-----LENGMIPTDTK 524
DB 443 LAGEBSPQGAERAKAPLANWGEPPSSSE 469

RESULT 12

US-09-431-367B-2
Query Match 29.4%; Score 812.5; DB 4; Length 393;
Best Local Similarity 53.8%; Pred. No. 1.5e-66;
Matches 157; Conservative 53; Mismatches 77; Indels 5; Gaps 3;
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

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/ FILE REFERENCE: MNI-074CP
/ CURRENT APPLICATION NUMBER: US/09/431,367B
/ CURRENT FILING DATE: 1999-11-01
/ PRIOR APPLICATION NUMBER: 09/259,951
/ PRIOR FILING DATE: 1999-03-01
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 499
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-431-367B-2

Query Match      17.5%; Score 483; DB 4; Length 499;
Best Local Similarity 25.8%; Pred. No. 6.9e-36;
Matches 131; Conservative 81; Mismatches 185; Indels 110; Gaps 14;

QY 79 VVYLVTGLVFRALQPESSQNTIALEKAEFLRDHVCVSPQLETLIQHALDADNAG 138
DB 12 IIFYLGAIAAIFVLEPHWKEAKQNYTKLHLLKEFFCLQGGDLKILEVSDAAGQ 71
QY 139 VSPIGNSSNHHWDLGSAFFPAGTIVTTIGYGNIAAPSTGGKIPCLYAIIFGIFLFG 198
DB 72 VALTGNQTFN--NWNPNAMIFAAVTTTIGYGNVAPKTPAGRLFCVFFGLGVPL---C 126
QY 199 LAGIGDQGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPAVIFKYI 258
DB 127 LTWII-SALGKFFGGRAKRLQQLTKRGVSLRKAQITCTVIFVWGLVHLVIPPVPMVT 185
QY 259 EGTWALIESYFVVVTTTGGDFVAGNAGINREWYKPLVFWFVLVGLAYFAAVLSMI 318
DB 186 EGNYYIEGLYSPITITIGDFVAGVNPNSANYHALYRYFVVELWYLGIA----- 236
QY 319 GDLRLVLSKTKKEVGEIKAHAAEWKANTVAEPRETRRLSVRIHDKLORAAATIRSMERR 378
DB 237 --WLSLF-----VNWKVS-----MFVEVHKAIK-----KRRRR 263
QY 379 RLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQBSINNRPNNRLK-----GP 428
DB 264 KESFESSPHSRKALQVKGSTASKDVNIFSLSKETYNLDLIQICKAMKTSGGGETGP 323
QY 429 -POLNKHGQ-----ASENIIKNGSTSRLLTKRKNKOLKLTLPED 468
DB 324 GFLGPGQGGLPALPFLVPLVYVKNRVPTLEVSQTLRSKHGVSRSPPDEAVARAPED 383
QY 469 VQIKYKTFNYSLEDEKKEB-----TEKMCNSDMSSTAMLTDC 507
DB 384 SSPAPEVFN--QLDRISBCEPDAQDYHPLIFQDASITFVWTEAGLSDEETSLSLEDN 442
QY 508 I-----QCHAE-----LENGMIPTDK 524
DB 443 LAGEESPQGAEAAPLNMGEPPSSSE 469

RESULT 13
US-09-236-080-4
Sequence 4, Application US/09236080
Patent No. 6242217
GENERAL INFORMATION:
APPLICANT: Helen Meadows
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-080-4
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Query Match      16.2%; Score 447; DB 3; Length 107;
Best Local Similarity 77.6%; Pred. No. 1.3e-33;
Matches 83; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 144 NSSNNSSHHWDLGSAFFPAGTIVTTIGYGNIAAPSTGGKIPCLYAIIFGIFLFG 203
DB 1 NSSQVSHWDLGSSFFPAGTIVTTIGFNGNISRTGGKIPCIYIALLGIFLFG 60
QY 204 DQGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTI 250
DB 61 DQGTIFGKIAKVEDTIFKNVSTKIRIISTIFILFGCVLFVAL 107

RESULT 14
US-08-749-816-2
Sequence 2, Application US/08749816
Patent No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunki, Michel
APPLICANT: Roney, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-2

Query Match      14.6%; Score 403; DB 3; Length 336;
Best Local Similarity 33.2%; Pred. No. 9.4e-29;
Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;

QY 76 FVVV--VVVLTGGLVFRALQPESSQNTIALEKAEFLRDHVCVSPQLETLIQHALD 133
DB 25 FLVGLYLLVFGAVVSSVELFYDLLQEKRLKRRFEEHECSEQLQELGRLVLE 84
QY 134 ADNAGVSPIGNSSNHHWDLGSAFFPAGTIVTTIGYGNIAAPSTGGKIPCLYAIIFG 193
DB 85 ASNYGVSVLSNAGN--WNWDFTSALFFASTVLTSTTGHTVPLSDGKAFCIYIVGIP 143
QY 194 LFGFLLAGIGDQGTIFGKSIARVEKVRKQV-----SQTIRVISTIL--PILA 242
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Db 144 FTLLFTAV-----VORITVHTRRPVLPHIRWGFSKQVVAIVHAVLLGFVT 192
QY 243 GCIVFTIPAVIFKIE-GWTALESYFVVVTLTTVGDFDVAGNAGINRYREWKPLVW 301
Db 193 SCFFP--IPAAVSVLEDDNLFESYFCFISLSTIGLDYVPEGYNOKFRELYKIGIT 250
QY 302 FWTVLGLAYFAAVLSMIGDMLRVLSK-----KTKEEVGEIKAAHAE 342
Db 251 CYLLGLGLIAMLVVLETCB-LHELKPKRMFYVKKDKDEQVHIIE 295

RESULT 15

US-09-144-914-2
; Sequence 2, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TWIK-1
US-09-144-914-2

Query Match 14.6%; Score 403; DB 3; Length 336;
Best Local Similarity 33.2%; Pred. No. 9.4e-29;
Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;
QY 76 FVVV--VYLVTCGLVFRALQPFESSQKNTIALEKAEFLRDHVCVSPQETLIQHLD 133
Db 25 FLVIGVLLYLVFGAVFSSVELPYEDLLROELKRLKRFLEEHECLSEQQLEQFLGRVLE 84
QY 134 ADNAGVSPIGNSNNSHNDLGSAPFFAGTVITIGYNIAPSTEGGKIPFCILYAFGIP 193
Db 85 ASNYGVSVLSNAGN--KNWDFTSALPFASVLTSTGVGHTVPLSDGSKAFCIYVIGIP 143
QY 194 LFGFLAGIGDQGTIFGKSIARVEKVKKKQV-----SQTKIRVISTIL--FILA 242
Db 144 FTLLFTAV-----VORITVHTRRPVLPHIRWGFSKQVVAIVHAVLLGFVT 192
QY 243 GCIVFTIPAVIFKIE-GWTALESYFVVVTLTTVGDFDVAGNAGINRYREWKPLVW 301
Db 193 SCFFP--IPAAVSVLEDDNLFESYFCFISLSTIGLDYVPEGYNOKFRELYKIGIT 250
QY 302 FWTVLGLAYFAAVLSMIGDMLRVLSK-----KTKEEVGEIKAAHAE 342
Db 251 CYLLGLGLIAMLVVLETCB-LHELKPKRMFYVKKDKDEQVHIIE 295

Search completed: April 28, 2005, 13:26:50
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:22:21 ; Search time 163 Seconds
(without alignments)
1276.547 Million cell updates/sec

Title: US-09-892-360-2
Perfect score: 2760
Sequence: 1 MFPLYTDFSLVAVPAAP.....IPTDTKDRPENSLLEDNRN 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_15Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2760	100.0	538	5	AAB47930
2	2760	100.0	538	5	AAB16596
3	2760	100.0	538	5	ABP69333
4	2697	97.7	543	5	AAB21804
5	2697	97.7	543	5	AAU81354
6	2697	97.7	543	5	AAU79472
7	2697	97.7	543	5	ABB83542
8	2697	97.7	543	6	ADA05746
9	2697	97.7	543	7	ADG08315
10	2697	97.7	543	8	ADN62310
11	2693	97.6	543	5	AAU79473
12	2657.5	96.3	724	5	AAO14193
13	1630	59.1	383	4	ABG02731
14	1412.5	51.2	557	4	ABG08305
15	1251.5	45.3	411	3	AAE10342
16	1251.5	45.3	422	7	ADP03575
17	1248.5	45.2	411	2	AAU28497
18	1247.5	45.2	370	2	AAU30648
19	1243	45.0	411	3	AAE10341
20	1242.5	45.0	411	2	AAU34133
21	1242.5	45.0	411	2	AAU28496
22	1242.5	45.0	411	4	ABE50044
23	1242.5	45.0	411	7	ADP03586
24	1242.5	45.0	411	8	ADQ76698
25	1235	44.7	411	5	AAE16597

26	1218.5	44.1	426	4	AAU07622	Aau07622 Human pot
27	1218.5	44.1	426	4	AAU07618	Aau07618 Human pot
28	1214.5	44.0	426	4	AAU07623	Aau07623 Human pot
29	1210.5	43.9	426	4	AAU07625	Aau07625 Human pot
30	1210.5	43.9	426	4	AAU07624	Aau07624 Human pot
31	1047	37.9	337	6	ABR41487	Abra41487 Human DIT
32	825.5	29.9	1314	4	AAU04571	Aau04571 Human G-P
33	825.5	29.9	1314	6	ABU60872	Abu60872 Human G-P
34	822.5	29.8	419	5	AAU78406	Aau78406 Amino aci
35	822.5	29.8	419	7	AAE38597	Aae38597 Human pot
36	822.5	29.8	419	7	ADK52550	Adk52550 Hematolog
37	822.5	29.8	419	8	ADH51639	Adh51639 Human 123
38	822.5	29.8	419	8	ADI27936	Adi27936 Human TWI
39	822.5	29.8	419	8	ADR44894	Adr44894 Polypepti
40	812.5	29.4	392	6	ABU60891	Abu60891 Human G-P
41	812.5	29.4	393	3	AAU94426	Aau94426 Human h-T
42	812.5	29.4	393	3	AAU94425	Aau94425 Human h-T
43	812.5	29.4	393	4	AAU67777	Aau67777 Human mec
44	790	28.6	398	2	AAU30647	Aau30647 A mechani
45	782	28.3	398	5	AAE16598	Aae16598 Human TWI

ALIGNMENTS

RESULT 1
AAB47930
ID AAB47930 standard; protein; 538 AA.

XX AC AAB47930;

XX DT 10-JUN-2002 (first entry)

XX DE Human TREK2.

KW Human; K+; channel; potassium; TREK2; pore domain; general anaesthetic;
KW neurotransmitter receptor.

XX OS Homo sapiens.

Key Domain	Location/Qualifiers
FT Domain	72..90
FT Domain	/note= "Membrane spanning domain 1"
FT Domain	152..175
FT Domain	/note= "Pore domain 1"
FT Domain	183..203
FT Domain	/note= "Membrane spanning domain 2"
FT Domain	234..255
FT Domain	/note= "Membrane spanning domain 3"
FT Domain	261..284
FT Domain	/note= "Pore domain 2"
FT Domain	300..319
FT Domain	/note= "Membrane spanning domain 4"

WO2002007115-A2.

03-JAN-2002.

27-JUN-2001; 2001WO-IB001436.

27-JUN-2000; 2000US-0214559P.

27-JUN-2001; 2001US-00892360.

(CNRS) CNRS CENT NAT RECH SCI.

Lazdunski M, Lesage F, Romey G;

WPI; 2002-139903/18.

N-PSDB; AAI72558.

New mammalian K+ channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anesthetic properties.

XX PS Claim 3; Page 44-46; 50pp; English.

XX CC This sequence shows a protein, which constitutes a human K⁺ channel, TREK2, which has two pore domains that produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K⁺ conditions. TREK2 is activated by general anaesthetics at clinical concentrations. It is modulated by different types of neurotransmitter receptors. The TREK2 gene produces a cDNA of 2730 bp which contains an open reading frame of 1617 nucleotides. The TREK2 protein has the same overall structure as previously described K⁺ channels. It has four membrane spanning domains (M1-M4), two pore domains (P1-P2) and an extended loop between M1 and P1. TREK2 shares 63% identity and 78% homology to TREK1. The chromosomal location of the TREK2 gene is 14q31.1. TREK2 is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties

XX SQ Sequence 538 AA;

Query Match 100.0%; Score 2760; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.7e-244;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLYTDFPLSLVAVFAAAPVCPQKSAATNGQPAPAPTPTPLSLSSSRATVVARMEGTSQ 60
 DB 1 MFPLYTDFPLSLVAVFAAAPVCPQKSAATNGQPAPAPTPTPLSLSSSRATVVARMEGTSQ 60

QY 61 GGLQTVMKWKTVAIFVWVYLVLTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120
 DB 61 GGLQTVMKWKTVAIFVWVYLVLTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120

QY 121 POELETLIQHALDADNAGVSPICGNSNNSSHHWDLGSAPFFAGTIVTTIGYNIAPSTEGG 180
 DB 121 POELETLIQHALDADNAGVSPICGNSNNSSHHWDLGSAPFFAGTIVTTIGYNIAPSTEGG 180

QY 181 KIFCILYALFGLIFGLLAGIGDQGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240
 DB 181 KIFCILYALFGLIFGLLAGIGDQGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240

QY 241 LAGCIVFTVPIAVIPKFIISGWTALSIYFVWVLTGTFGDFVAGNAGINREWKPLV 300
 DB 241 LAGCIVFTVPIAVIPKFIISGWTALSIYFVWVLTGTFGDFVAGNAGINREWKPLV 300

QY 301 WFWILVGLAYFAVLISMGIDMLRVLSKTKVEEVEIKAAAEKAWNTAEFEETRRLSV 360
 DB 301 WFWILVGLAYFAVLISMGIDMLRVLSKTKVEEVEIKAAAEKAWNTAEFEETRRLSV 360

QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRP 420
 DB 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRP 420

QY 421 NNLRKGPQLNKGCGASEDNIINFGSTSLTKRKNKDLKTLPEDEVOKIYKTPRNTS 480
 DB 421 NNLRKGPQLNKGCGASEDNIINFGSTSLTKRKNKDLKTLPEDEVOKIYKTPRNTS 480

QY 481 LDEEKKREETERKCNDSNSTAMLTDCIOQHAELNGMLPTDKREPENNILLDRN 538
 DB 481 LDEEKKREETERKCNDSNSTAMLTDCIOQHAELNGMLPTDKREPENNILLDRN 538

RESULT 2
 ID AAE16596
 AC AAE16596; standard; protein; 538 AA.
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Human TWIK-Related K⁺ channel-2 (TREK-2) protein.
 XX
 KW Human; TWIK-Related K⁺ Channel-2; TREK-2; anaesthetic; chromosome 14q31; screening.

XX OS Homo sapiens.

XX FH Key

FT Region Location/Qualifiers
 72..90
 /note= "M1 membrane spanning segment"

FT Domain
 152..175
 /note= "p1 pore domain"

FT Region
 183..203
 /note= "M2 membrane spanning segment"

FT Region
 234..255
 /note= "M3 membrane spanning segment"

FT Domain
 261..284
 /note= "p2 pore domain"

FT Region
 300..319
 /note= "M4 membrane spanning segment"

XX WO200200715-A2.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-IB001436.

XX 27-JUN-2000; 2000US-0214559P.

XX 27-JUN-2001; 2001US-00892360.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Romey G;
 WPI; 2002-139903/18.
 N-PSDB; AAD27459.

XX New mammalian K⁺ channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anaesthetic properties.

XX Claim 3; Page 45-47; 50pp; English.

XX The invention relates to a mammalian K⁺ channel protein with two pore domains, called TREK2 (TWIK-Related K⁺ Channel). The protein produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K⁺ conditions. TREK2 is a member of the fatty acid-activated and mechanosensitive K⁺ channel family. TREK-2 gene located on chromosome 14q31 is abundantly expressed in kidney, pancreas and moderately in testis, brain, colon and small intestine. The mammalian K⁺ channel protein is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties. The present sequence is human TREK-2 protein

XX SQ Sequence 538 AA;

Query Match 100.0%; Score 2760; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.7e-244;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLYTDFPLSLVAVFAAAPVCPQKSAATNGQPAPAPTPTPLSLSSSRATVVARMEGTSQ 60
 DB 1 MFPLYTDFPLSLVAVFAAAPVCPQKSAATNGQPAPAPTPTPLSLSSSRATVVARMEGTSQ 60

QY 61 GGLQTVMKWKTVAIFVWVYLVLTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120
 DB 61 GGLQTVMKWKTVAIFVWVYLVLTGGLVFRALBOPFESSQKNTALEKAEFLRDHVCVS 120

QY 121 POELETLIQHALDADNAGVSPICGNSNNSSHHWDLGSAPFFAGTIVTTIGYNIAPSTEGG 180
 DB 121 POELETLIQHALDADNAGVSPICGNSNNSSHHWDLGSAPFFAGTIVTTIGYNIAPSTEGG 180

QY 181 KIFCILYALFGLIFGLLAGIGDQGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240
 DB 181 KIFCILYALFGLIFGLLAGIGDQGTIFGKSIARVEKVFRRKQVSOQTKIRVISTILFI 240

QY 241 LAGCIVFTVTPAVIPKIVIGTWTALSIYFVVVTLTTVGDFGVAGNAGINREWKPLV 300
DB 241 LAGCIVFTVTPAVIPKIVIGTWTALSIYFVVVTLTTVGDFGVAGNAGINREWKPLV 300
QY 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAAHAEWKANVTAFRETRRLSV 360
DB 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAAHAEWKANVTAFRETRRLSV 360
QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
DB 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
QY 421 NNLRKGPQLNKGQGASEDNIIKFGSTSRLTGKKNKDLKKTLPEDVQKIYKTFRNYS 480
DB 421 NNLRKGPQLNKGQGASEDNIIKFGSTSRLTGKKNKDLKKTLPEDVQKIYKTFRNYS 480
QY 481 LDEKKKEETEKKMCSNDSNSTAMLTDCIQOHALENGMIPTDTKDRPENNSLLEDNRN 538
DB 481 LDEKKKEETEKKMCSNDSNSTAMLTDCIQOHALENGMIPTDTKDRPENNSLLEDNRN 538

RESULT 3
ABP69333
ID ABP69333 standard; protein; 538 AA.
XX AC ABP69333;
XX DT 20-JAN-2003 (first entry)
XX DE Human polypeptide SEQ ID NO 1380.
XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cystostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX OS Homo sapiens.
XX FN WO200270539-A2.
XX PD 12-SEP-2002.
XX PF 05-MAR-2002; 2002WO-US005095.
XX PR 05-MAR-2001; 2001US-00799451.
XX PA (HYSEQ-) HYSEQ INC.
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QH, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
DR WPI; 2002-759812/82.
DR N-PSDB; ABZ11550.
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX Claim 9; SEQ ID NO 1380; 1012pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP69302-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical

CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 538 AA;

Query Match 100.0%; Score 2760; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.7e-244; Indels 0; Gaps 0;
Matches 538; Conservative 0; Mismatches 0;
QY 1 MFPLYTDFPLSLVAVPAAAPVCPKSAATNGQPAPPTPRLSSISRRATVVARMEGTSQ 60
DB 1 MFPLYTDFPLSLVAVPAAAPVCPKSAATNGQPAPPTPRLSSISRRATVVARMEGTSQ 60
QY 61 GGLQTVMKWKTVAIFVAVVAVVYLVVTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVS 120
DB 61 GGLQTVMKWKTVAIFVAVVAVVYLVVTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVS 120
QY 121 POELETLLIOHALDADNAGVSPIGNSSNNSHWDLGSAFFAGTAVLTIGYGNIAPESTEGS 180
DB 121 POELETLLIOHALDADNAGVSPIGNSSNNSHWDLGSAFFAGTAVLTIGYGNIAPESTEGS 180
QY 181 KIFCILYAIPIGPIPLGFLLAGIGDQIGTIFGKSIARVEKVFRRKQVSOVKIRVISTILFI 240
DB 181 KIFCILYAIPIGPIPLGFLLAGIGDQIGTIFGKSIARVEKVFRRKQVSOVKIRVISTILFI 240
QY 241 LAGCIVFTVTPAVIPKIVIGTWTALSIYFVVVTLTTVGDFGVAGNAGINREWKPLV 300
DB 241 LAGCIVFTVTPAVIPKIVIGTWTALSIYFVVVTLTTVGDFGVAGNAGINREWKPLV 300
QY 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAAHAEWKANVTAFRETRRLSV 360
DB 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEVGEIKAAHAEWKANVTAFRETRRLSV 360
QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
DB 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNR 420
QY 421 NNLRKGPQLNKGQGASEDNIIKFGSTSRLTGKKNKDLKKTLPEDVQKIYKTFRNYS 480
DB 421 NNLRKGPQLNKGQGASEDNIIKFGSTSRLTGKKNKDLKKTLPEDVQKIYKTFRNYS 480
QY 481 LDEKKKEETEKKMCSNDSNSTAMLTDCIQOHALENGMIPTDTKDRPENNSLLEDNRN 538
DB 481 LDEKKKEETEKKMCSNDSNSTAMLTDCIQOHALENGMIPTDTKDRPENNSLLEDNRN 538

RESULT 4
AAE21804
ID AAE21804 standard; protein; 543 AA.
XX AC AAE21804;
XX DT 16-JUL-2002 (first entry)
XX DE Human TREK2 protein.
XX KW Human; hTREK2 protein; cancer; diabetes; pulmonary disease; asthma;
KW cardiovascular disease; inflammatory disease; psychiatric disorder;
KW renal disease; neurodegenerative disease; neurological disorder;
KW Alzheimer's disease; depression; schizophrenia; stroke; vaccine; trauma;
XX pain.
XX OS Homo sapiens.
XX FN GB2365010-A.
XX

PD 13-FEB-2002.
XX
XX
XX 24-APR-2001; 2001GB-00010129.
XX
XX 25-APR-2000; 2000GB-00010060.
PR 01-JUN-2000; 2000GB-00013370.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Chapman CG, Duckworth DM;
XX
XX WPI; 2002-332557/37.
DR N-PSDB; AAD34451.
XX
XX Novel human TREK2 (HTREK2) polypeptide and polynucleotide encoding it,
PT useful for identifying agonists and antagonists in the treatment of
PT diseases associated with a HTREK2 imbalance, such as diabetes, cancers or
PT asthma.
XX
XX Claim 1; Page 21-22; 29pp; English.
XX
XX The invention relates to human HTREK2 polypeptides and nucleic acid
CC molecules encoding such polypeptides. TREK2 polypeptides are useful in
CC screening assays to identify compounds that may stimulate or inhibit
CC their function or level of expression. Sequences of the invention are
CC used to treat cancer, diabetes, asthma, pulmonary disease, cardiovascular
CC diseases, inflammatory disease, renal disease, pain, psychiatric
CC disorders including depression and schizophrenia, neurodegenerative
CC disease including Alzheimer's disease, stroke and head trauma and
CC neurological disorders. They are also used as vaccines. The present
CC sequence is human HTREK2 protein
XX
XX Sequence 543 AA;
SQ

Query Match 97.7%; Score 2697; DB 5; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.1e-238;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 VAVPAAAPVCPKSAATGPPAPPTPTPLSLSSRATVVARMEGTSQGLQVTKWKV 72
DB 18 VAVPAAAPVCPKSAATGPPAPPTPTPLSLSSRATVVARMEGTSQGLQVTKWKV 77
QY 73 VAIFVVVVVLTGVLFRALQEPFESSQNTIALEKAEFLRDHVCVSPQELTLIQHAL 132
DB 78 VAIFVVVVVLTGVLFRALQEPFESSQNTIALEKAEFLRDHVCVSPQELTLIQHAL 137
QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVTTTGYGNIAPSTGGKIFCLLYAIFGI 192
DB 138 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVTTTGYGNIAPSTGGKIFCLLYAIFGI 197
QY 193 PLFGFLLAGIGDGLTIFGKSTARVEKVRKKQVSTKIRVSTILFILAGCIVFTTIPA 252
DB 198 PLFGFLLAGIGDGLTIFGKSTARVEKVRKKQVSTKIRVSTILFILAGCIVFTTIPA 257
QY 253 VIFKYEIETGTALESIFVVTTLTTVGFGDFVAGNAGINRYREWKPLVFWILVGLAYFA 312
DB 258 VIFKYEIETGTALESIFVVTTLTTVGFGDFVAGNAGINRYREWKPLVFWILVGLAYFA 317
QY 313 AVLSMIGDWLRLVSKTKVEVGBIKAHAAEWKANVTABPRTTRRLSVRIHDKLQAAAT 372
DB 318 AVLSMIGDWLRLVSKTKVEVGBIKAHAAEWKANVTABPRTTRRLSVRIHDKLQAAAT 377
QY 373 RSMERRRLGIDRAHSLDMLSPKRSVFAALDTGRFKASSQSINNRPNNRLKGPQLN 432
DB 378 RSMERRRLGIDRAHSLDMLSPKRSVFAALDTGRFKASSQSINNRPNNRLKGPQLN 437
QY 433 KHGQGAASEDNIINKFSTSRLLTKRKNKDLKLTLPEDVQKIYKTFRNYSDDEKKEBETEK 492
DB 438 KHGQGAASEDNIINKFSTSRLLTKRKNKDLKLTLPEDVQKIYKTFRNYSDDEKKEBETEK 497
QY 493 MCNSDSSSTAMLTDCITQOHAELNGMIPDTDKREPENNSLLEDNRN 538
|||||

DB 498 MCNSDSSSTAMLTDCITQOHAELNGMIPDTDKREPENNSLLEDNRN 543
RESULT 5
AAU81354
ID AAU81354 standard; protein; 543 AA.
XX
XX AAU81354;
XX
XX 09-APR-2002 (first entry)
XX
XX Novel human ion channel protein #34.
DE XX
XX Human; ion channel; anti-HIV; analgesic; cytostatic; antidiabetic;
KW anorectic; metabolic; hypertensive; hypotensive; thrombolytic; cardiac;
KW antiatherosclerotic; neuroleptic; antimigraine; antiparkinsonian;
KW tranquiliser; antidepressant; neuroprotective; anticonvulsant; pain;
KW antinflammatory; antirheumatic; antithrombotic; immunosuppressive;
KW antipsoriatic; antiasthmatic; vulnary; asthma; traumatic brain injury;
KW psychiatric disorder; gene therapy; asthma; cancer; diabetes; anorexia;
KW human immunodeficiency virus; HIV-1; HIV-2; cancer; diabetes; anorexia;
KW myocardial infarction; Parkinson's disease; schizophrenia; anxiety;
KW dementia; Huntington's disease; thyroid disorder; inflammation;
KW autoimmune disorder; hormonal disorder; renal failure; psoriasis;
KW movement disorder.
XX
XX Homo sapiens.
OS
XX WO200185788-A2.
PN
XX 15-NOV-2001.
PD
XX
XX 10-MAY-2001; 2001WO-US014965.
PF
XX
XX 10-MAY-2000; 2000US-0203305P.
PR 23-MAY-2000; 2000US-0206526P.
PR 25-MAY-2000; 2000US-0207033P.
PR 25-MAY-2000; 2000US-0207092P.
PR 25-MAY-2000; 2000US-0207093P.
PR 07-JUL-2000; 2000US-0216893P.
PR 04-AUG-2000; 2000US-0223245P.
PR 04-OCT-2000; 2000US-0237873P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
PA
XX
XX Roberts SL, Benjamin CW, Karnovsky AM, Ruble CL;
PI
XX
XX WPI; 2002-062237/08.
DR N-PSDB; ABK27503.
XX
XX New polynucleotides, useful for identifying ion channel activity
PT modulators that are used for treating Parkinson's disease, schizophrenia,
PT migraine, anxiety, manic depression, encodes the ion channel polypeptide.
XX
XX Claim 2; Page 89; 172pp; English.
PS
XX
XX The invention relates to an isolated nucleic acid molecule (I) which
CC encodes a novel ion channel protein, ion-x (II). The nucleic acid,
CC protein and antibody are useful for identifying a compound which binds a
CC nucleic acid molecule encoding ion-x. These are useful for treatment of a
CC neurological or psychiatric disorder which modulates ligand binding to
CC ion-x in neurons of the mammal; in gene therapy to restore ion-x activity
CC in certain disease states; for treating asthma traumatic brain injury,
CC etc; modulators of ion-x activity or expression are useful for treating
CC diseases such as viral infections caused by human immunodeficiency virus
CC (HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,
CC hypertension, atherosclerosis, thrombosis, myocardial infarction,
CC cardiomyopathies, arteriosclerosis, Parkinson's disease, schizophrenia,
CC migraine, anxiety, manic depression, dementia, Huntington's disease,
CC thyroid disorders, inflammatory conditions, rheumatoid arthritis, and
CC autoimmune disorders, hormonal disorders, renal failure, psoriasis, and
CC movement disorders. AAU81321-AAU81360 represent human ion channel protein
CC sequences of the invention

XX Sequence 543 AA;
SQ

Query Match
Best Local Similarity 97.7%; Score 2697; DB 5; Length 543;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 72
DB 18 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 77

QY 73 VAIFVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
DB 78 VAIFVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137

QY 133 DADNAGVSPIGNSSNNSSHWDLSGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILVAIFGI 192
DB 138 DADNAGVSPIGNSSNNSSHWDLSGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILVAIFGI 197

QY 193 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQTKIRVISTILFILAGCIVFVTIPA 252
DB 198 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQTKIRVISTILFILAGCIVFVTIPA 257

QY 253 VIFKYIEGWTALSIYFVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 312
DB 258 VIFKYIEGWTALSIYFVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 317

QY 313 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWNTAEFRETTRRLSVEIHDKLQRAATI 372
DB 318 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWNTAEFRETTRRLSVEIHDKLQRAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQSSINNRPNRLKGPQQLN 432
DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQSSINNRPNRLKGPQQLN 437

QY 433 KHGQASDNIINKGTSRLTKRKNKDLKTLPEDEVQKIYKTFPNYSLDEKKEETEK 492
DB 438 KHGQASDNIINKGTSRLTKRKNKDLKTLPEDEVQKIYKTFPNYSLDEKKEETEK 497

QY 493 MCNSDNSTAMLTDCIQHAELENGMIPTDTKOREPENNLSLEDNRN 538
DB 498 MCNSDNSTAMLTDCIQHAELENGMIPTDTKOREPENNLSLEDNRN 543

RESULT 6

AAU79472
ID AAU79472 standard; protein; 543 AA.

XX AC AAU79472;

XX 15-JUL-2002 (first entry)

XX Human novel transporter protein.

XX Human; transporter; transgenic; transporter mediated disease;
KW drug screening; pharmacogenomic analysis; chromosome 18.

XX Homo sapiens.

XX WO200224748-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US029211.

XX 19-SEP-2000; 2000US-0233663P.

XX 06-DEC-2000; 2000US-00729920.

XX (PEKE) PE CORP NY.

XX Guegler K, Ketchum KA, Di Francesco V, Beasley EM;

XX WPI; 2002-351999/38.

DR

DR N-PSDB; ABK49585, ABK49586.

XX New human transporter proteins and nucleic acids, useful as models in the
PT development of human therapeutic agents, in identifying therapeutic
PT proteins, or as query sequence in database searches to identify related
PT sequences.

XX Claim 1; Fig 2; 207pp; English.

XX The invention relates to a new isolated peptide being a human transporter
CC protein, an allelic variant, orthologue, fragment or sequence that is 70%
CC homologous to the transporter. Also included are a nucleic acid encoding
CC the transporter (including allelic variants, orthologue, fragment or
CC complement), an antibody against the protein, a gene chip comprising the
CC nucleic acids, a transgenic non-human animal comprising the nucleic
CC acids, a nucleic acid vector comprising the nucleic acids, a host cell
CC containing the vector, identifying agents that bind to and/or modulate
CC the function of the transporter, and treating a disease or condition
CC mediated by a human transporter protein by administering to the patient
CC an identified agent or modulator. The peptide sequences and the nucleic
CC acid sequences encoding these peptides can be used as models for the
CC development of human therapeutic targets, aid in the identification of
CC therapeutic proteins, and serve as targets for the development of human
CC therapeutic agents that modulate transporter activity in cells and
CC tissues that express the transporter. These sequences may also be used as
CC query sequence in database searches to identify other family members or
CC related sequences. The proteins may be used to raise antibodies or to
CC elicit immune response; as a reagent in assays designed to quantitatively
CC determine protein levels in biological fluids; as markers for tissues in
CC which the corresponding protein is expressed; in drug screening assays in
CC cell-based or cell-free systems; to identify compounds that modulate
CC transporter activity of the protein in its natural state or altered form
CC that causes a specific disease or pathology associated with the
CC transporter; as target for diagnosing a disease or predisposition to
CC disease mediated by the peptide; and in pharmacogenomic analysis. The
CC nucleic acids are useful as hybridisation probes or primers; in
CC monitoring the effectiveness of modulating compounds on the expression or
CC activity of the transporter gene in clinical trials or treatment regimen;
CC in diagnostic assays for qualitative changes in transporter nucleic acid
CC expression; and as antisense constructs. The gene for the transporter is
CC located on chromosome 18. The present sequence represents the novel human
CC transporter

XX Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 5; Length 543;

Best Local Similarity 100.0%; Pred. No. 1.1e-238;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 72
DB 18 VAVPAAAPVCPKSAATNGQPPAPAPPTPTPLRSLSSRATVVARMEGTSQGLQTVMKWKTIV 77

QY 73 VAIFVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
DB 78 VAIFVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137

QY 133 DADNAGVSPIGNSSNNSSHWDLSGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILVAIFGI 192
DB 138 DADNAGVSPIGNSSNNSSHWDLSGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILVAIFGI 197

QY 193 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQTKIRVISTILFILAGCIVFVTIPA 252
DB 198 PLFGFLLAGIGDQLTIFGKSIARVEKVRKQVQTKIRVISTILFILAGCIVFVTIPA 257

QY 253 VIFKYIEGWTALSIYFVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 312
DB 258 VIFKYIEGWTALSIYFVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 317

QY 313 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWNTAEFRETTRRLSVEIHDKLQRAATI 372
DB 318 AVLSMIGDNLRLVLSKTKKEVGEIKAAHAEKAWNTAEFRETTRRLSVEIHDKLQRAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRNNLRLKGPQLN 432
 Db 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRNNLRLKGPQLN 437
 QY 433 KHGQASDNIINKFGSTSRITKRNKDKLTLPEDVQKIYKTFPNYSILDEKKEEETK 492
 Db 438 KHGQASDNIINKFGSTSRITKRNKDKLTLPEDVQKIYKTFPNYSILDEKKEEETK 497
 QY 493 MCNSDSSSTAMLTDCIQHAELNGMIPTDTKREPENNLSLEDNRN 538
 Db 498 MCNSDSSSTAMLTDCIQHAELNGMIPTDTKREPENNLSLEDNRN 543
 RESULT 7
 ABB83542
 ID ABB83542 standard; protein; 543 AA.
 AC ABB83542;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Hypothalamus-expressed potassium channel protein.
 XX
 KW Hypothalamus; potassium channel; obesity; human.
 XX
 OS Homo sapiens.
 OS
 PN WO200252000-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 25-DEC-2001; 2001WO-JP011330.
 XX
 PR 26-DEC-2000; 2000JP-00396020.
 XX
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 XX
 PI Yokoi H, Inamura K, Sano Y, Miyake A, Mochizuki S;
 XX
 DR WPI, 2002-508889/54.
 DR N-PSDB; ABN85879.
 XX
 PT Hypothalamus-expressed potassium channel protein and encoded
 PT polynucleotide, applicable in screening inhibitors as anti-obestic agents
 PT to control food intake and enhanced energy consumption.
 XX
 PS Claim 1; Page 39-41; 45pp; Japanese.
 XX
 CC This invention relates to a hypothalamus-expressed protein having
 CC potassium channel activity. The protein and polynucleotide are applicable
 CC in screening inhibitors as anti-obesity agents to control food intake and
 CC enhanced energy consumption. The said screening process is advantageous
 CC as it is convenient to operate. This sequence represents a potassium
 CC channel activity protein
 XX
 SQ Sequence 543 AA;
 Query Match 97.7%; Score 2697; DB 5; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.1e-238; Indels 0; Gaps 0;
 Matches 526; Conservative 0; Mismatches 0;
 QY 13 VAVPAAAPVCPKSNATNGOPAPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKTIV 72
 Db 18 VAVPAAAPVCPKSNATNGOPAPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKTIV 77
 QY 73 VAIFVVVVYLVGTGLVFRALRQPESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
 Db 78 VAIFVVVVYLVGTGLVFRALRQPESSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137
 QY 133 DADNAGVSPIGNSSNNSHWDIGSAFFPAGTIVTTIGYNIAPSTEGGKIFCILYAFGI 192
 Db 138 DADNAGVSPIGNSSNNSHWDIGSAFFPAGTIVTTIGYNIAPSTEGGKIFCILYAFGI 197

QY 193 PLFGLLAGIDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTILFLAGCIVFVTIPA 252
 Db 198 PLFGLLAGIDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTILFLAGCIVFVTIPA 257
 QY 253 VIFKYISGWTALBSIYFVWVTLTTVVGSDPFVAGNAGINREWKPLVFWILVGLAYPA 312
 Db 258 VIFKYISGWTALBSIYFVWVTLTTVVGSDPFVAGNAGINREWKPLVFWILVGLAYPA 317
 QY 313 AVLSMIGDMLRVLSKTKKEEVEGEIKAHAAEWKANTVAFRETRRRRLSVIEIHDKLQRAATI 372
 Db 318 AVLSMIGDMLRVLSKTKKEEVEGEIKAHAAEWKANTVAFRETRRRRLSVIEIHDKLQRAATI 377
 QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRNNLRLKGPQLN 432
 Db 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRNNLRLKGPQLN 437
 QY 433 KHGQASDNIINKFGSTSRITKRNKDKLTLPEDVQKIYKTFPNYSILDEKKEEETK 492
 Db 438 KHGQASDNIINKFGSTSRITKRNKDKLTLPEDVQKIYKTFPNYSILDEKKEEETK 497
 QY 493 MCNSDSSSTAMLTDCIQHAELNGMIPTDTKREPENNLSLEDNRN 538
 Db 498 MCNSDSSSTAMLTDCIQHAELNGMIPTDTKREPENNLSLEDNRN 543
 RESULT 8
 ADA05746
 ID ADA05746 standard; protein; 543 AA.
 AC ADA05746;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV19a protein SEQ ID NO:106.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 OS
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.

PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patursajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort I, Gorman L, Zernhusen BD, Anderson DW, Zhong M, Catterton B;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2003-381626/36.
 DR N-PSDB; ADA05745.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 PT
 XX Claim 1; Page 176; 586pp; English.
 PS
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, neuroprotective, antiparkinsonian
 CC and antilipemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 543 AA;
 Query Match 97.7%; Score 2697; DB 6; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.1e-238;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 13 VAVFAAPVCPKATNGQPPAPAPTPTPLRISIRATVVARMEGTSQGLQTVMKKTV 72
 18 VAVFAAPVCPKATNGQPPAPAPTPTPLRISIRATVVARMEGTSQGLQTVMKKTV 77
 73 VAIFVVVVVYLVLTGGLVFRALFQPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 132

DB 78 VAIFVVVVVYLVLTGGLVFRALFQPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 137
 QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTVTTTGYGNIAPSTEGGKIFCILYAIFGI 192
 DB 138 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTVTTTGYGNIAPSTEGGKIFCILYAIFGI 197
 QY 193 PLFGLLAGIGDQGLCTIFGKSTARVEKVPKQVQTKIRVISTTILFILAGCIVFTTIPA 252
 DB 198 PLFGLLAGIGDQGLCTIFGKSTARVEKVPKQVQTKIRVISTTILFILAGCIVFTTIPA 257
 QY 253 VIFKIEGTALLESYFVWVLTITTVGDFVAGNAGINRYRWYKPLVWFWILVGLAYFA 312
 DB 258 VIFKIEGTALLESYFVWVLTITTVGDFVAGNAGINRYRWYKPLVWFWILVGLAYFA 317
 QY 313 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLRSVEIHDKQRAATI 372
 DB 318 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLRSVEIHDKQRAATI 377
 QY 373 RSMERRRGLDQRAHSLDMLSPKESVFAALDTGTFKASSQESINNRPNRLKGPQOLN 432
 DB 378 RSMERRRGLDQRAHSLDMLSPKESVFAALDTGTFKASSQESINNRPNRLKGPQOLN 437
 QY 433 KHGQGASEDNIIKFGSTSRITKKNKDLKKTLPEDVOKIYKTFRNYSLDESKRETEK 492
 DB 438 KHGQGASEDNIIKFGSTSRITKKNKDLKKTLPEDVOKIYKTFRNYSLDESKRETEK 497
 QY 493 MCNSDNSSTAMLTDCIQHAELENGMIPTDKREPENNSLLEDNRN 538
 DB 498 MCNSDNSSTAMLTDCIQHAELENGMIPTDKREPENNSLLEDNRN 543

RESULT 9

ADE08315
 ID ADE08315 standard; protein; 543 AA.
 XX
 AC ADE08315;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel protein (useful for identifying genetic disorders) #470.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX
 FN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002MO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0385384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 22-APR-2002; 2002US-0372615P.
 PR 24-APR-2002; 2002US-00128558.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI: 2003-569235/53.
 DR N-PSDB; ADE07404.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

PS Claim 20; SEQ ID NO 1381; 1177pp; English.

The invention comprises the amino acid and coding sequences of novel proteins, the DNA and protein sequences of the invention are useful markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.

AX Sequence 543 AA;

Query Match	97.7%; Score 2697; DB 7; Length 543;
Best Local Similarity	100.0%; Pred. No. 1.1e-238;
Matches	526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	13 VAVPAAAPVCPKATNGCPAPAPATPTPRLSISSRATVVARMEGTSQGLQTMWKWKT 72
DB	18 VAVPAAAPVCPKATNGCPAPAPATPTPRLSISSRATVVARMEGTSQGLQTMWKWKT 77
QY	73 VAFVFWVVVYLVLTGGLVFRALEQPFESSOKNTIALEKAEFLRDHVCVSPQSELTLIQHAL 132
DB	78 VAFVFWVVVYLVLTGGLVFRALEQPFESSOKNTIALEKAEFLRDHVCVSPQSELTLIQHAL 137
QY	133 DADNAGVSPIGNSSNNSSHMDLGSAPFPAGTVITTIYGYNTIAPSTEGGKIFCILYAIAPGI 192
DB	138 DADNAGVSPIGNSSNNSSHMDLGSAPFPAGTVITTIYGYNTIAPSTEGGKIFCILYAIAPGI 197
QY	193 PLRFLAGIDGDLGTIFGKSIARVEKVKRQVQSOTKIRIVISITLPLACIVFVTIPA 252
DB	198 PLRFLAGIDGDLGTIFGKSIARVEKVKRQVQSOTKIRIVISITLPLACIVFVTIPA 257
QY	253 VIFKYIEGWTALESIYFVVVTLTTVFGDFVAGGNAGINRYREWKPLVFWFVILVGLAYFA 312
DB	258 VIFKYIEGWTALESIYFVVVTLTTVFGDFVAGGNAGINRYREWKPLVFWFVILVGLAYFA 317
QY	313 AVLSMIGDWLRVLKTKTKEEYGEIKAHAAEWKANVTAEFRTRRLRSVEIHDKLQRAATI 372
DB	318 AVLSMIGDWLRVLKTKTKEEYGEIKAHAAEWKANVTAEFRTRRLRSVEIHDKLQRAATI 377
QY	373 RSMERRRLGLDORAHSLDMLSPKRSVFPAALDTGRFKASSOESINNRPNNLRLKGPEQLN 432
DB	378 RSMERRRLGLDORAHSLDMLSPKRSVFPAALDTGRFKASSOESINNRPNNLRLKGPEQLN 437
QY	433 KHGQGAASEDNIINKFGSTSRLTKRKNQDLKKTLPEDVQKIYKTFPNYSLDSEKKEEETEK 492
DB	438 KHGQGAASEDNIINKFGSTSRLTKRKNQDLKKTLPEDVQKIYKTFPNYSLDSEKKEEETEK 497
QY	493 MCNSDNSSTAMLTDCIOAHLENGMIPTDTKOREPENNSLLEDNRN 538
DB	498 MCNSDNSSTAMLTDCIOAHLENGMIPTDTKOREPENNSLLEDNRN 543

RESULT 10

RESULT 10
ADN62910

ADN62910 :
ID ADN62910 standard; protein; 543 AA.

ADN62910:

01-JUL-2004 (first entry)

XX DE Human NOV 1993

XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.

XX OS Homo sapiens.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

US2004038223-A1.	XX	PN
	XX	PD
26- FEB- 2004.	XX	PD
	XX	PD
01-OCT-2002; 2002US-00262511.	XX	PD
02-OCT-2001; 2001US-0326483P.	XX	PD
03-OCT-2001; 2001US-0327435P.	XX	PD
05-OCT-2001; 2001US-0327449P.	XX	PD
09-OCT-2001; 2001US-0327917P.	XX	PD
09-OCT-2001; 2001US-0328024P.	XX	PD
09-OCT-2001; 2001US-0328044P.	XX	PD
09-OCT-2001; 2001US-0328056P.	XX	PD
12-OCT-2001; 2001US-0328489P.	XX	PD
15-OCT-2001; 2001US-0329414P.	XX	PD
17-OCT-2001; 2001US-0330142P.	XX	PD
18-OCT-2001; 2001US-0330309P.	XX	PD
22-OCT-2001; 2001US-0341058P.	XX	PD
24-OCT-2001; 2001US-0332668P.	XX	PD
24-OCT-2001; 2001US-0343629P.	XX	PD
29-OCT-2001; 2001US-0349575P.	XX	PD
01-NOV-2001; 2001US-0346357P.	XX	PD
17-APR-2002; 2002US-0373260P.	XX	PD
19-APR-2002; 2002US-0373815P.	XX	PD
19-APR-2002; 2002US-0373817P.	XX	PD
19-APR-2002; 2002US-0373826P.	XX	PD
19-APR-2002; 2002US-0373884P.	XX	PD
22-APR-2002; 2002US-0374977P.	XX	PD
16-MAY-2002; 2002US-0381037P.	XX	PD
16-MAY-2002; 2002US-0381038P.	XX	PD
16-MAY-2002; 2002US-0381042P.	XX	PD
17-MAY-2002; 2002US-0381042P.	XX	PD
28-MAY-2002; 2002US-0383656P.	XX	PD
23-MAY-2002; 2002US-0383831P.	XX	PD
25-JUN-2002; 2002US-0391335P.	XX	PD
	XX	PD
(SMIT/ SMITHSON G.	PA	PA
(MILL/ MILLET I.	PA	PA
(PEYM/ PEYMAN J A.	PA	PA
(KEGU/ KUKUDA R.	PA	PA
(JUNG/ JU J.	PA	PA
(LILL/ LI L.	PA	PA
(GUOX/ GUO X.	PA	PA
(PATI/ PATIRAJAN M.	PA	PA
(SPYT/ SPYTEK K A.	PA	PA
(EDIN/ EDINGER S R.	PA	PA
(ELLE/ ELLERMAN K.	PA	PA
(MALY/ MALYANKAR U M.	PA	PA
(ORTT/ ORT T.	PA	PA
(GORM/ GORMAN L.	PA	PA
(ZERR/ ZERHUSEN B D.	PA	PA
(ANDE/ ANDERSON D W.	PA	PA
(ZHON/ ZHONG M.	PA	PA
(CATV/ CARTERTON E.	PA	PA
(JIWV/ JI W.	PA	PA
(MILL/ MILLER C B.	PA	PA
(RAST/ RASTELLI L.	PA	PA
(STON/ STONE D J.	PA	PA
(PENA/ PENA C E A.	PA	PA
(SHEN/ SHENOY S G.	PA	PA
(SHIM/ SHIMKETS R A.	PA	PA
(ROTH/ ROTHENBERG M E.	PA	PA
(LEAC/ LEACH M D.	PA	PA
(AGEE/ AGEE M L.	PA	PA
(BERG/ BERGS C.	PA	PA
(DIPI/ DIPIPO V A.	PA	PA
(EISE/ EISEN A.	PA	PA
(GANG/ GANGOLLI E A.	PA	PA
(RIEG/ RIEGER D K.	PA	PA
(SPAD/ SPADERNA S K.	PA	PA

XX OS Homo sapiens.

PI Patturajan M, Spytek KA, Bainger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerkhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shency SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI; 2004-213931/20.
 DR N-PSDB; ADN62909.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 XX diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX Claim 1; SEQ ID NO.106; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 8; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.1e-238;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 13 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKTIV 72
 18 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKTIV 77
 73 VAIFVVVVVYLTGVLFPALQPFSSQKNTIALEKAEFLDHVQVSPQLETLIQHAL 132
 78 VAIFVVVVVYLTGVLFPALQPFSSQKNTIALEKAEFLDHVQVSPQLETLIQHAL 137
 133 DADNAGVSPIGNSSNNSWDLGSAPFFAGTVTTIGYGNIAAPSTEGGKIFCILVAIRGI 192
 138 DADNAGVSPIGNSSNNSWDLGSAPFFAGTVTTIGYGNIAAPSTEGGKIFCILVAIRGI 197
 193 PLFGFLLAGIGDQLGTIFGKSIAARVEKVFRRKQVSTKIRLVISTILFILAGCIVFVTIPA 252
 198 PLFGFLLAGIGDQLGTIFGKSIAARVEKVFRRKQVSTKIRLVISTILFILAGCIVFVTIPA 257
 253 VIFKIEGHTALESIFVVTITTVGFGDFVAGNAGINRYRWYKPLVFWFVLVGLAYPA 312
 258 VIFKIEGHTALESIFVVTITTVGFGDFVAGNAGINRYRWYKPLVFWFVLVGLAYPA 317
 313 AVLSMIGDLRLVLSKTKKEVGEIKAAHAEWKNYTAERETRLRSVEIHDKLOAAATI 372
 318 AVLSMIGDLRLVLSKTKKEVGEIKAAHAEWKNYTAERETRLRSVEIHDKLOAAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQBSINNRPNRLRKGPEQLN 432
 Db |||||
 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQBSINNRPNRLRKGPEQLN 437
 QY 433 KKGQGAASEDNIINKFGSTSRLLTKRKNKOLKKTLPEDVQKIYKTFRNYSLDEEKCBEETEK 492
 Db |||||
 438 KKGQGAASEDNIINKFGSTSRLLTKRKNKOLKKTLPEDVQKIYKTFRNYSLDEEKCBEETEK 497
 QY 493 MCNSDSSSTAMLTDCICQHAELNGMIPDTDKOREPENNSLLEDRN 538
 Db |||||
 498 MCNSDSSSTAMLTDCICQHAELNGMIPDTDKOREPENNSLLEDRN 543

RESULT 11

AAU79473

ID AAU79473 standard; protein; 543 AA.

AC AAU79473;

DT 15-JUL-2002 (first entry)

DE Human novel transporter protein variant.

KW Human; transporter; transgenic; transporter mediated disease;
 XX drug screening; pharmacogenomic analysis; chromosome 18.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 233

FT /note= "Wild-type Gln substituted by Lys"

PN WO200224748-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US029211.

XX 19-SEP-2000; 2000US-0233663P.

XX 06-DEC-2000; 2000US-00729920.

XX (PEXE) PE CORP NY.

XX Guegler K, Ketchum KA, Di Francesco V, Beasley EM;

XX WPI; 2002-351999/38.

XX New human transporter proteins and nucleic acids, useful as models in the
 PT development of human therapeutic agents, in identifying therapeutic
 PT proteins, or as query sequence in database searches to identify related
 PT sequences.

XX Disclosure; Page; 207pp; English.

XX The invention relates to a new isolated peptide being a human transporter
 CC protein, an allelic variant, orthologue, fragment or sequence that is 70%
 CC homologous to the transporter. Also included are a nucleic acid encoding
 CC the transporter (including allelic variants, orthologue, fragment or
 CC complement), an antibody against the protein, a gene chip comprising the
 CC nucleic acids, a transgenic non-human animal comprising the nucleic
 CC acids, a nucleic acid vector comprising the nucleic acids, a host cell
 CC containing the vector, identifying agents that bind to and/or modulate
 CC the function of the transporter, and treating a disease or condition
 CC mediated by a human transporter protein by administering to the patient
 CC an identified agent or modulator. The peptide sequences and the nucleic
 CC acid sequences encoding these peptides can be used as models for the
 CC development of human therapeutic targets, aid in the identification of
 CC therapeutic proteins, and serve as targets for the development of human
 CC therapeutic agents that modulate transporter activity in cells and
 CC tissues that express the transporter. These sequences may also be used as
 CC query sequence in database searches to identify other family members or
 CC related sequences. The proteins may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively

CC determine protein levels in biological fluids; as markers for tissues in
 CC which the corresponding protein is expressed; in drug screening assays in
 CC cell-based or cell-free systems; to identify compounds that modulate
 CC transporter activity of the protein in its natural state or altered form
 CC that causes a specific disease or pathology associated with the
 CC transporter; as target for diagnosing a disease or predisposition to
 CC disease mediated by the peptide; and in pharmacogenomic analysis. The
 CC nucleic acids are useful as hybridisation probes or primers; in
 CC monitoring the effectiveness of modulating compounds on the expression or
 CC activity of the transporter gene in clinical trials or treatment regimen;
 CC in diagnostic assays for qualitative changes in transporter nucleic acid
 CC expression; and as antisense constructs. The gene for the transporter is
 CC located on chromosome 18. The present sequence represents a variant of
 CC the novel human transporter. Note: The present sequence is not shown in
 CC the specification but was created by the indexer from the information in
 CC figure 3 and the transporter sequence appearing as AAU79472

XX SQ Sequence 543 AA;

Query Match 97.6%; Score 2693; DB 5; Length 543;
 Best Local Similarity 99.8%; Pred. No. 2.5e-238;
 Matches 525; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 72
 DB 18 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 77

QY 73 VAIFVVVVVYLTGGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
 DB 78 VAIFVVVVVYLTGGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137

QY 133 DADNAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYNIAPSTEGGKIFCLYIAIFI 192
 DB 138 DADNAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYNIAPSTEGGKIFCLYIAIFI 197

QY 193 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 252
 DB 198 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 257

QY 253 VIFKYIEGWTALIESIYFVVVTLTITVGFDPVAGNAGINRYEYKPLVFWFVLGLAYFA 312
 DB 258 VIFKYIEGWTALIESIYFVVVTLTITVGFDPVAGNAGINRYEYKPLVFWFVLGLAYFA 317

QY 313 AVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTRRLSVETIHDKLRAT 372
 DB 318 AVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTRRLSVETIHDKLRAT 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP 432
 DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP 437

QY 433 KHQCGASEDNINKFGSTSLTRKNDLKKTIPEVQKIYKTFRNYSLDEEKKBEETEK 492
 DB 438 KHQCGASEDNINKFGSTSLTRKNDLKKTIPEVQKIYKTFRNYSLDEEKKBEETEK 497

QY 493 MCNSDNSSTAMLTDCIQOHAELNGMPTDTKDREPENNSLLDRN 538
 DB 498 MCNSDNSSTAMLTDCIQOHAELNGMPTDTKDREPENNSLLDRN 543

RESULT 12

AAO14193
 ID AAO14193 standard; protein; 724 AA.

XX AC AAO14193;

CC 03-MAY-2002 (first entry)

XX DE Human transporter and ion channel TRICH-10.

XX KW Human; transporter and ion channel; TRICH; transport disorder;
 KW neurological disorder; muscle disorder; immunological disorder;
 KW cell proliferative disorder; neuroprotective; nootropic;

KW cerebroprotective; immunosuppressive; cytostatic; respiratory; muscular;
 KW gene therapy.

XX OS Homo sapiens.

XX WO200204520-A2.

XX 17-JAN-2002.

XX 05-JUL-2001; 2001WO-US021448.

XX 07-JUL-2000; 2000US-0216547P.

XX 14-JUL-2000; 2000US-0218232P.

XX 21-JUL-2000; 2000US-0220112P.

XX 28-JUL-2000; 2000US-0221839P.

XX (INCY-) INCYTE GENOMICS INC.

XX RAumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;

XX Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang J;

XX Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;

XX Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azimzai Y, Lal P;

XX Elliott VS, Nguyen DB, Xu Y, Seilhamer JU, Borowsky ML, Khan FA;

XX Kearney L, Thangavelu K, Das D, Policky JL;

XX WPI; 2002-205969/26.

XX N-PSDB; AAL44676.

XX New human transporters and ion channel polypeptides for diagnosing,
 XX treating or preventing transport, neurological, muscle, immunological and
 XX cell proliferative disorders.

XX Claim 1; Page 158-160; 230pp; English.

XX The present invention provides the protein and coding sequences of a
 XX number of human transporters and ion channel proteins, designated TRICH-1-
 XX TRICH-32. The sequences can be used in the treatment of transport,
 XX neurological, muscle, immunological and cell proliferative disorders. The
 XX present sequence is a protein of the invention

XX SQ Sequence 724 AA;

Query Match 96.3%; Score 2657.5; DB 5; Length 724;
 Best Local Similarity 98.7%; Pred. No. 7e-235;
 Matches 523; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY 13 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 72
 DB 196 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSISSRATVVARMEGTSQGLQTVMKWKT 255

QY 73 VAIFVVVVVYLTGGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132
 DB 256 VAIFVVVVVYLTGGLVFRALPEPSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 315

QY 133 DADNAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYNIAPSTEGGKIFCLYIAIFI 192
 DB 316 DADNAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYNIAPSTEGGKIFCLYIAIFI 374

QY 193 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 252
 DB 375 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFVTIPA 434

QY 253 VIFKYIEGWTALIESIYFVVVTLTITVGFDPVAGNAGINRYEYKPLVFWFVLGL 308
 DB 435 VIFKYIEGWTALIESIYFVVVTLTITVGFDPVAGNAGINRYEYKPLVFWFVLGL 494

QY 309 AYFAAVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTRRLSVETIHDKLR 368
 DB 495 AYFAAVLSMIGDMLRVLSKTKKEVGEIKAAAEWKANVTAEFRTRRLSVETIHDKLR 554

QY 369 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP 428
 DB 555 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGP 614

QY 429 EQLNKHGQASDNIINKFGSTSRLLTKRKNKOLKKTLPEDVQKIYKTFNYSLSDEKKEE 488
 DB 615 EQLNKHGQASDNIINKFGSTSRLLTKRKNKOLKKTLPEDVQKIYKTFNYSLSDEKKEE 674
 QY 489 ETEKMCNSDNTAMLTDCIQHAELENGMIPDTTKDREPENNSLLEDNRN 538
 DB 675 ETEKMCNSDNTAMLTDCIQHAELENGMIPDTTKDREPENNSLLEDNRN 724

RESULT 13

ABG02731
 ID ABG02731 standard; protein; 383 AA.

XX AC
 XX ABG02731;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #2722.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS66918.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 33090; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG03077 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 383 AA;

Query Match 59.1%; Score 1630; DB 4; Length 383;

Best Local Similarity 100.0%; Pred. No. 8.8e-141;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 RKQVQSQTIRVISTILFILACGIVFVTIPAVIFKYIEGWTALSIYFVVVTLTTVGFGD 281

DB 67 RKQVQSQTIRVISTILFILACGIVFVTIPAVIFKYIEGWTALSIYFVVVTLTTVGFGD 126

QY 282 FVAGGNAGINREWKPLVWFILVGLAYFAAVALSMIGDMLVLSKTKKEEVEIKAHAA 341

DB 127 FVAGGNAGINREWKPLVWFILVGLAYFAAVALSMIGDMLVLSKTKKEEVEIKAHAA 186

QY 342 EWKANVTAEFRTRRLRSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKKSQVFA 401

DB 187 EWKANVTAEFRTRRLRSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKKSQVFA 246

QY 402 ALDTCRPFKASSQESSINRPNNRLKGPOLNKHGQASDNIINKFGSTSRLLTKRKNKOL 461

DB 247 ALDTCRPFKASSQESSINRPNNRLKGPOLNKHGQASDNIINKFGSTSRLLTKRKNKOL 306

QY 462 KKTLPEDVQKIYKTFNYSLSDEKKEEETKMCNSDNTAMLTDCIQHAELENGMIP 521

DB 307 KKTLPEDVQKIYKTFNYSLSDEKKEEETKMCNSDNTAMLTDCIQHAELENGMIP 366

QY 522 DTKDREPENNSLLEDNRN 538

DB 367 DTKDREPENNSLLEDNRN 383

RESULT 14

ABG08305

ID ABG08305 standard; protein; 557 AA.

XX AC ABG08305;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #8296.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS72492.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 38664; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is

RESULT 15	
AAE10342	
ID	AAE10342 standard; protein; #11 AA.
XX	
AC	AAE10342;
XX	
DT	10-DEC-2001 (first entry)
XX	
DE	Murine TREK-1 potassium channel protein.
DE	
KW	Murine; potassium channel protein; TREK-1; anaesthetic; analgesia; amnesia.
KW	
XX	
OS	Mus musculus.
XX	
PN	WO200047738-A2.
XX	
PD	17-AUG-2000.
XX	
PF	11-FEB-2000; 2000WO-IB000226.
XX	
PR	12-FEB-1999; 99US-0119727P.
PR	11-FEB-2000; 2000US-00503089.

Search completed: April 28, 2005, 13:25:15
Job time : 166 secs

Search completed: April 28, 2005, 13:25:15
Job time : 166 secs

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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:26:07 ; Search time 134 Seconds
(without alignments)
1337.396 Million cell updates/sec

Title: US-09-892-360-2
Perfect score: 2760
Sequence: 1 MFLLYDFFLSLVAVPAAP.....IPTDKREPENSLLEDNRN 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2760	100.0	538	11	US-09-892-360-2
2	2697	97.7	526	9	US-09-729-920-4
3	2697	97.7	543	9	US-09-729-920-2
4	2697	97.7	543	10	US-09-852-386-73
5	2697	97.7	543	14	US-10-332-175-2
6	2697	97.7	543	15	US-10-262-511-106
7	2657.5	96.3	724	15	US-10-332-447-10
8	2560.5	92.8	538	9	US-09-729-920-5
9	1248.5	45.2	411	9	US-09-828-746-6
10	1243	45.0	411	11	US-09-892-360-18
11	1242.5	45.0	411	9	US-09-828-746-2
12	1242.5	45.0	411	14	US-10-121-746-83
13	1242.5	45.0	411	16	US-10-745-210-2

14	1238.5	44.9	370	9	US-09-939-484-8	Sequence 8, Appli
15	1238.5	44.9	370	9	US-09-939-483-8	Sequence 8, Appli
16	1218.5	44.1	426	8	US-08-816-011-45	Sequence 45, Appl
17	1218.5	44.1	426	17	US-10-870-492-45	Sequence 57, Appl
18	1218.5	44.1	426	17	US-10-870-492-57	Sequence 58, Appl
19	1214.5	44.0	426	17	US-10-870-492-59	Sequence 59, Appl
20	1210.5	43.9	426	17	US-10-870-492-60	Sequence 60, Appl
21	1210.5	43.9	426	17	US-10-870-492-60	Sequence 29, Appl
22	825.5	29.9	1314	9	US-09-747-835A-29	Sequence 2, Appli
23	825.5	29.9	1314	15	US-10-312-312-29	Sequence 2, Appli
24	822.5	29.8	419	9	US-09-828-035-2	Sequence 44, Appl
25	822.5	29.8	419	14	US-10-345-680-44	Sequence 29, Appl
26	822.5	29.8	419	14	US-10-146-733-29	Sequence 8, Appli
27	822.5	29.8	419	15	US-10-352-684A-8	Sequence 19, Appl
28	822.5	29.8	419	15	US-10-331-399-19	Sequence 55, Appl
29	812.5	29.4	392	9	US-09-747-835A-55	Sequence 2, Appli
30	812.5	29.4	392	15	US-10-312-312-55	Sequence 55, Appl
31	812.5	29.4	392	14	US-10-243-035-2	Sequence 2, Appli
32	790	28.6	398	11	US-09-892-360-19	Sequence 19, Appl
33	610.5	22.1	421	15	US-10-276-774-2599	Sequence 2599, Ap
34	512	18.6	294	13	US-10-121-566-2	Sequence 2, Appli
35	512	18.6	294	15	US-10-451-892-2	Sequence 2, Appli
36	512	18.6	294	15	US-10-459-190-2	Sequence 2, Appli
37	512	18.6	294	15	US-10-459-190-9	Sequence 9, Appli
38	512	18.6	309	15	US-10-080-334-172	Sequence 172, App
39	512	18.6	309	15	US-10-080-334-177	Sequence 177, App
40	511	18.5	239	15	US-10-459-190-11	Sequence 11, Appl
41	511	18.5	292	15	US-10-451-892-6	Sequence 6, Appli
42	511	18.5	292	15	US-10-451-892-10	Sequence 10, Appl
43	511	18.5	292	15	US-10-459-190-4	Sequence 4, Appli
44	483	17.5	499	9	US-09-735-169A-2	Sequence 2, Appli
45	483	17.5	499	9	US-09-735-171A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-892-360-2
Sequence 2, Application US/09892360
Publication No. US20040101833A1
GENERAL INFORMATION:
APPLICANT: LAZDUNSKI, MICHAEL
APPLICANT: LESAGE, FLORENCE
APPLICANT: RONEY, GEORGES
TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
TITLE OF INVENTION: RILUZOLE
FILE REFERENCE: 1256-R-00
CURRENT APPLICATION NUMBER: US/09/892,360
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 60/214,559
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-892-360-2

Query Match 100.0%; Score 2760; DB 11; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.7e-216;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFLLYDFFLSLVAVPAAPVCPKSNATNGOPPAPPTPTPTLSISRRATVVARMEGTSQ 60
Dy 1 MFLLYDFFLSLVAVPAAPVCPKSNATNGOPPAPPTPTPTLSISRRATVVARMEGTSQ 60
Qy 61 GGLQTMKMTVAIFVWVYLVGTGLVFRALPEQPPESSQKNTIALEKAEFLRDHVCVS 120
Dy 61 GGLQTMKMTVAIFVWVYLVGTGLVFRALPEQPPESSQKNTIALEKAEFLRDHVCVS 120

QY 121 POELETLIQHALDADNAGVSPICGNSNNSSHDLSGSAFFAGTAVTTTIGYGNIAFSTEGG 180
DB 121 POELETLIQHALDADNAGVSPICGNSNNSSHDLSGSAFFAGTAVTTTIGYGNIAFSTEGG 180
QY 181 KIFCILYAIIFGFLPGLAGIDGOLGTTIFGKSIARVEKVFPRKQVSTQKIRVISTILFI 240
DB 181 KIFCILYAIIFGFLPGLAGIDGOLGTTIFGKSIARVEKVFPRKQVSTQKIRVISTILFI 240
QY 241 LAGCIVFVTIPAVIFKYIEGWTALSIYFVVVTLTTVGGDFVAGNAGINREWKPLV 300
DB 241 LAGCIVFVTIPAVIFKYIEGWTALSIYFVVVTLTTVGGDFVAGNAGINREWKPLV 300
QY 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSV 360
DB 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSV 360
QY 361 EIHDKLORAAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTRGFKASSQESINNR 420
DB 361 EIHDKLORAAATIRSMERRRGLDORAHSLDMLSPKRSVFAALDTRGFKASSQESINNR 420
QY 421 NNLRLKGPOLNKHGQASEDNIIKFGSTSLTKRKNKDLKTLPEDEVOKIYKTFRNY 480
DB 421 NNLRLKGPOLNKHGQASEDNIIKFGSTSLTKRKNKDLKTLPEDEVOKIYKTFRNY 480
QY 481 LDEEKKKEETERMCMNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 538
DB 481 LDEEKKKEETERMCMNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 538

RESULT 2

US-09-729-920-4
; Sequence 4, Application US/09729920
; Patent No. US20020103115A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Human
US-09-729-920-4

Query Match 97.7%; Score 2697; DB 9; Length 526;
Best Local Similarity 100.0%; Pred. No. 4.9e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSLSSSRATVARMGTSQGLQTVMKWKT 72
DB 1 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSLSSSRATVARMGTSQGLQTVMKWKT 60
QY 73 VAI FVVVVVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 132
DB 61 VAI FVVVVVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 120
QY 133 DADNAGVSPIGNSSNNSSHDLSGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 192
DB 121 DADNAGVSPIGNSSNNSSHDLSGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 180
QY 193 PLFGFLLAGIGDQGTIFGKSIARVEKVFPRKQVSTQKIRVISTILFILAGCIVFTI 252
DB 181 PLFGFLLAGIGDQGTIFGKSIARVEKVFPRKQVSTQKIRVISTILFILAGCIVFTI 240
QY 253 VIFKYIEGWTALSIYFVVVTLTTVGGDFVAGNAGINREWKPLVFWILVGLAYFA 312
DB 241 VIFKYIEGWTALSIYFVVVTLTTVGGDFVAGNAGINREWKPLVFWILVGLAYFA 300

QY 313 AVLSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIHDKLQRAATI 372
DB 301 AVLSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIHDKLQRAATI 360
QY 373 RSMERRRGLDORAHSLDMLSPKRSVFAALDTRGFKASSQESINNRPNLRLKGPOLN 432
DB 361 RSMERRRGLDORAHSLDMLSPKRSVFAALDTRGFKASSQESINNRPNLRLKGPOLN 420
QY 433 KHGQASADNIIKFGSTSLTKRKNKDLKTLPEDEVOKIYKTFRNYSLDEEKKKEET 492
DB 421 KHGQASADNIIKFGSTSLTKRKNKDLKTLPEDEVOKIYKTFRNYSLDEEKKKEET 480
QY 493 MCNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 538
DB 481 MCNSDSTAMLTDCIQOHAELNGMIPTDTKOREPENNSLLEDN 526

RESULT 3

US-09-729-920-2
; Sequence 2, Application US/09729920
; Patent No. US20020103115A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Human
US-09-729-920-2

Query Match 97.7%; Score 2697; DB 9; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSLSSSRATVARMGTSQGLQTVMKWKT 72
DB 18 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSLSSSRATVARMGTSQGLQTVMKWKT 77
QY 73 VAI FVVVVVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 132
DB 78 VAI FVVVVVYLVGTGLVFRALQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 137
QY 133 DADNAGVSPIGNSSNNSSHDLSGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 192
DB 138 DADNAGVSPIGNSSNNSSHDLSGSAFFAGTAVTTTIGYGNIAFSTEGGKIFCILYAI 197
QY 193 PLFGFLLAGIGDQGTIFGKSIARVEKVFPRKQVSTQKIRVISTILFILAGCIVFTI 252
DB 198 PLFGFLLAGIGDQGTIFGKSIARVEKVFPRKQVSTQKIRVISTILFILAGCIVFTI 257
QY 253 VIFKYIEGWTALSIYFVVVTLTTVGGDFVAGNAGINREWKPLVFWILVGLAYFA 312
DB 258 VIFKYIEGWTALSIYFVVVTLTTVGGDFVAGNAGINREWKPLVFWILVGLAYFA 317
QY 313 AVLSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIHDKLQRAATI 372
DB 318 AVLSMIGDMLRVLSKTKKEEVEIKAHAAEWKANTVAFRETRRLSVIHDKLQRAATI 377
QY 373 RSMERRRGLDORAHSLDMLSPKRSVFAALDTRGFKASSQESINNRPNLRLKGPOLN 432
DB 378 RSMERRRGLDORAHSLDMLSPKRSVFAALDTRGFKASSQESINNRPNLRLKGPOLN 437
QY 433 KHGQASADNIIKFGSTSLTKRKNKDLKTLPEDEVOKIYKTFRNYSLDEEKKKEET 492
DB 438 KHGQASADNIIKFGSTSLTKRKNKDLKTLPEDEVOKIYKTFRNYSLDEEKKKEET 497

QY 493 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 543

RESULT 4

US-09-852-386-73
; Sequence 73, Application US/09852386
; Publication No. US20030064433A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Rubie, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00133.US1
; CURRENT APPLICATION NUMBER: US/09/852,386
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,305
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/207,092
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/206,526
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,033
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,093
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/216,893
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/207,873
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/223,245
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 73
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-386-73

Query Match 97.7%; Score 2697; DB 10; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISIRATVVARMEGTSGGLQTVNMKKT 72
DB 18 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISIRATVVARMEGTSGGLQTVNMKKT 77

QY 73 VAVFVVVVVYLVGTGLVFRALQEPPESSOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 132
DB 78 VAVFVVVVVYLVGTGLVFRALQEPPESSOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 137

QY 133 DADNAGVSPIGNSSNNSHWDLGSAFFAGTVITIGYGNIAAPSTEGGKIFCILYAI 192
DB 138 DADNAGVSPIGNSSNNSHWDLGSAFFAGTVITIGYGNIAAPSTEGGKIFCILYAI 197

QY 193 PLFGFLLAGIDGQITIFGKSIARVEKVRKQVSQTKIRVISTILFILAGCIVFVTIPA 252
DB 198 PLFGFLLAGIDGQITIFGKSIARVEKVRKQVSQTKIRVISTILFILAGCIVFVTIPA 257

QY 253 VIFKYIEGWTALLESYFVVVVTITVVGDFVAGGNAGINREWKPLVFWFVLVGLAYFA 312
DB 258 VIFKYIEGWTALLESYFVVVVTITVVGDFVAGGNAGINREWKPLVFWFVLVGLAYFA 317

QY 313 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLSVEIHDKQRAATI 372
DB 318 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLSVEIHDKQRAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQOLN 432
DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQOLN 437

QY 493 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 543

RESULT 6
US-10-262-511-106
; Sequence 106, Application US/10262511

QY 433 KHGOGASEDNIIKFGSTSRITKRNKDKLKTLPEDVQKIYKTFPNYSLDEKKEEETEK 492
DB 438 KHGOGASEDNIIKFGSTSRITKRNKDKLKTLPEDVQKIYKTFPNYSLDEKKEEETEK 497

QY 493 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 543

RESULT 5

US-10-332-175-2
; Sequence 2, Application US/10332175
; Publication No. US20030176342A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20030176342A1:el potassium channel
; FILE REFERENCE: Y013PCT-666
; CURRENT APPLICATION NUMBER: US/10/332,175
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: JP 2000-396020
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-175-2

Query Match 97.7%; Score 2697; DB 14; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISIRATVVARMEGTSGGLQTVNMKKT 72
DB 18 VAVPAAAPVCPKSNATNGQPPAPAPPTPTPLRISIRATVVARMEGTSGGLQTVNMKKT 77

QY 73 VAVFVVVVVYLVGTGLVFRALQEPPESSOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 132
DB 78 VAVFVVVVVYLVGTGLVFRALQEPPESSOKNTIALEKAEFLRDHVCVSPQLETLIOHAL 137

QY 133 DADNAGVSPIGNSSNNSHWDLGSAFFAGTVITIGYGNIAAPSTEGGKIFCILYAI 192
DB 138 DADNAGVSPIGNSSNNSHWDLGSAFFAGTVITIGYGNIAAPSTEGGKIFCILYAI 197

QY 193 PLFGFLLAGIDGQITIFGKSIARVEKVRKQVSQTKIRVISTILFILAGCIVFVTIPA 252
DB 198 PLFGFLLAGIDGQITIFGKSIARVEKVRKQVSQTKIRVISTILFILAGCIVFVTIPA 257

QY 253 VIFKYIEGWTALLESYFVVVVTITVVGDFVAGGNAGINREWKPLVFWFVLVGLAYFA 312
DB 258 VIFKYIEGWTALLESYFVVVVTITVVGDFVAGGNAGINREWKPLVFWFVLVGLAYFA 317

QY 313 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLSVEIHDKQRAATI 372
DB 318 AVLSMIGDMLRVLSKTKKEEVEIKAAHAAEWKANTVAFRETRRLSVEIHDKQRAATI 377

QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQOLN 432
DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLKGPQOLN 437

QY 433 KHGOGASEDNIIKFGSTSRITKRNKDKLKTLPEDVQKIYKTFPNYSLDEKKEEETEK 492
DB 438 KHGOGASEDNIIKFGSTSRITKRNKDKLKTLPEDVQKIYKTFPNYSLDEKKEEETEK 497

QY 493 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 538
DB 498 MCNSDSSSTAMLTDCIQQAELNGLMPTDTKDRPENNSLLEDNRN 543

Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkete, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 106
LENGTH: 543
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-106

Query Match 97.7%; Score 2697; DB 15; Length 543;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13 VAVPAAAPVCPKSAATGPPAPPTPTPLSTSSRATVVARMEGTSQGLQTVMKWKTIV 72
18 VAVPAAAPVCPKSAATGPPAPPTPTPLSTSSRATVVARMEGTSQGLQTVMKWKTIV 77
73 VAIFVVVVVLTGGLVFRALFQPPSSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 132

RESULT 7

US-10-332-447-10
Sequence 10, Application US/10332447
Publication No. US20040053258A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
APPLICANT: TANG, Y. Tom; HARLAND, Lee; BURFORD, Neil;
APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine R.;
APPLICANT: WALIA, Narinder K.; AU-YOUNG, Janice;
APPLICANT: WALSH, Roderick T.; RAMKUMAR, Jayalaxmi;
APPLICANT: LU, Yan; LU, Dyung Aina M.; AZIMZAI, Yalda;
APPLICANT: LAL, Preeti; ELLIOTT, Vicki S.; NGUYEN, Dannel B.;
APPLICANT: XU, Yuming; SEILHAMER, Jeffrey J.; BOROWSKY, Mark L.;
APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELU, Kavitha;
APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-0149 USN
CURRENT APPLICATION NUMBER: US/10/332,447
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/216,547
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/218,232
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/220,112
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/221,839
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 724
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040053258A1 7472728CDI
US-10-332-447-10

Query Match 96.3%; Score 2657.5; DB 15; Length 724;
Best Local Similarity 98.7%; Pred. No. 1.3e-207;
Matches 523; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY 13 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSISRRATVVARMEGTSGGLQTVMKWKT 72
DB 196 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSISRRATVVARMEGTSGGLQTVMKWKT 255

QY 73 VAVFVVVVYLVGTGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHAL 132
DB 256 VAVFVVVVYLVGTGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHAL 315

QY 133 DADNAGVSPIGNSSNNSSHDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILIYAFGI 192
DB 316 DADNAGVSPIGNSSNNSSHDLSGAPFPAGTIVTTM-YGNIAPSTEGKIFCILIYAFGI 374

QY 193 PLFGFLLAGIGDQGTIFGKSTARVEKVRKKQVSTQKIRVISTILFILAGCIVFVTIPA 252
DB 375 PLFGFLLAGIGDQGTIFGKSTARVEKVRKKQVSTQKIRVISTILFILAGCIVFVTIPA 434

QY 253 VIFKYIEGTALLESYFVVVTLTTVGFDFVA---GGNAGINRYREWKPLVFWFVLVGL 308
DB 435 VIFKYIEGTALLESYFVVVTLTTVGFDFVAVVVFRGNAGINRYREWKPLVFWFVLVGL 494

QY 309 AYFAAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQR 368
DB 495 AYFAAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQR 554

QY 369 AATRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGP 428
DB 555 AATRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGP 614

QY 429 EQLKNGGQASSEDNIINKFGSTSLTKRKNKDLKKTLPEDVOKIYKTFRNTSLDEKKEE 488
DB 615 EQLKNGGQASSEDNIINKFGSTSLTKRKNKDLKKTLPEDVOKIYKTFRNTSLDEKKEE 674

QY 489 ETERKMSDSSSTAMLTDCIQOHAELNGMIPTDTKDRPENNSLLEDN 538
DB 675 ETERKMSDSSSTAMLTDCIQOHAELNGMIPTDTKDRPENNSLLEDN 724

RESULT 8
US-09-729-920-5
; Sequence 5, Application US/09729920
; Patent No. US20020103115A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CLO00858
; CURRENT APPLICATION NUMBER: US/09/729,920
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-729-920-5

Query Match 92.8%; Score 2560.5; DB 9; Length 538;
Best Local Similarity 95.4%; Pred. No. 6.8e-200;
Matches 503; Conservative 9; Mismatches 8; Indels 7; Gaps 2;

QY 13 VAVPAAAPVCPKSAATNGQPPAPPTPTPLRSISRRATVVARMEGTSGGLQTVMKWKT 71
DB 18 VAVPAAAPVCPKSAATNGH-----HFVPLRSISRRATVVARMEGTSGGLQTVMKWKT 71

QY 72 VAVFVVVVYLVGTGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHA 131
DB 72 VAVFVVVVYLVGTGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHA 131

QY 132 LDADNAGVSPIGNSSNNSSHDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILIYAFGI 191
DB 132 LDADNAGVSPIGNSSNNSSHDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILIYAFGI 191

QY 192 IPLFGFLLAGIGDQGTIFGKSTARVEKVRKKQVSTQKIRVISTILFILAGCIVFVTIP 251
DB 192 IPLFGFLLAGIGDQGTIFGKSTARVEKVRKKQVSTQKIRVISTILFILAGCIVFVTIP 251

QY 252 AVIFKYIEGTALLESYFVVVTLTTVGFDFVAGNAGINRYREWKPLVFWFVLVGLAYF 311
DB 252 AVIFKYIEGTALLESYFVVVTLTTVGFDFVAGNAGINRYREWKPLVFWFVLVGLAYF 311

QY 312 AAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQRAAT 371
DB 312 AAVLSMIGDMLRVLSKKTKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQRAAT 371

QY 372 IRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGP 431
DB 372 IRSERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGP 431

QY 432 NKHGQASSEDNIINKFGSTSLTKRKNKDLKKTLPEDVOKIYKTFRNTSLDEKKEE 491
DB 432 NKHGQASSEDNIINKFGSTSLTKRKNKDLKKTLPEDVOKIYKTFRNTSLDEKKEE 491

QY 492 KVCNSDSSSTAMLTDCIQOHAELNGMIPTDTKDRPENNSLLEDN 538
DB 492 KVCNSDSSSTAMLTDCIQOHAELNGMIPTDTKDRPENNSLLEDN 538

RESULT 9
US-09-828-746-6
; Sequence 6, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

Query Match 45.2%; Score 1248.5; DB 9; Length 411;
Best Local Similarity 64.3%; Pred. No. 4.5e-93;
Matches 247; Conservative 53; Mismatches 67; Indels 17; Gaps 5;

QY 17 AAAPVCPKSAATNGQPPAPPTPTPLRSISRRATVVA-RMEGTSGGLQTVMKWKTVAI 75
DB 2 AAPDLLDPKSA-----AQNSKPLSPSPKPTVLASRVESDS---AINVMKWKTVSTI 50

QY 76 FVVVVVYLVGTGLVFRALBQPFSSQKNTIALEKAEFLDRHVCVSPQLETLIQHALDAD 135
DB 51 FLVVVLLIITGAAVFKALEQFQISQRTTIVIQKTFIAQHACVNSTELDELIQIVAAI 110

QY 136 NAGVSPIGNSSNNSSHDLSGAPFPAGTIVTTIGYNIAPSTEGKIFCILIYAFGI 195
DB 111 NAGLPIGNSNQVSHWDLGSSFFAGTIVTTIGYNIAPSTEGKIFCILIYAFGI 170

QY 196 GFLLAGIGDQGTIFGKSTARVEKVRKKQVSTQKIRVISTILFILAGCIVFVTIP 255
DB 196 GFLLAGIGDQGTIFGKSTARVEKVRKKQVSTQKIRVISTILFILAGCIVFVTIP 255

Db 171 GFLLAGVGDQGTIFGKGIARVEDTFKWNVSQTKIRIISTITIFILFGCVLFPALPAVIF 230
QY 256 KYIEGWTALSIYFVVVTLTTVGFGDFVAGGNAGINREWKYPLVWFWLVLGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDYFYPVWFWLVLGLAYFAAVL 289
QY 316 SMIGDMLRVLSKTKKEVEGEIKAAHAAEWKANTVAETFRTRRLSVIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEVEGEFRAHAAEWANTVAETFKETRRLSVIHDKLOAAATIRSM 346
QY 376 ERRRLGLDORAHSLDMLSPKRSV 399
Db 347 -KRKLSAELAGNHQELTFCMRTL 369

RESULT 10

US-09-892-360-18
; Sequence 18, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMEY, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-892-360-18

Query Match 45.0%; Score 1243; DB 11; Length 411;
Best Local Similarity 62.7%; Pred. No. 1.3e-92;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;
QY 17 AAPVCQPKSATNGOPPAPAPTPTPLRSLSSRATVVA-RMEGTSQGLQTVWKKTVVAI 75
Db 2 RAPDLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKWKTVSTI 50
QY 76 FVVVVVLTGVLFPALQEPFESSQKNTTALAEFLRDHVCVSPQELTILQHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKTFISQHSVCNSTELDELIIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHDGLSAPFPAGTVTTTIGYGNIAPISTETILFAGCIVFTTIPAVIF 195
Db 111 NAGIIPLGNTSNOISHDGLSSFPFAGTVTTTIGFNGISPRTEGGKIFCIIYALLGIPLF 170
QY 196 GFLLAGIGDQGTIFGKGIARVEDTFKWNVSQTKIRIISTITIFILAGCIVFTTIPAVIF 255
Db 171 GFLLAGVGDQGTIFGKGIARVEDTFKWNVSQTKIRIISTITIFILFGCVLFPALPAVIF 230
QY 256 KYIEGWTALSIYFVVVTLTTVGFGDFVAGGNAGINREWKYPLVWFWLVLGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDYFYPVWFWLVLGLAYFAAVL 289
QY 316 SMIGDMLRVLSKTKKEVEGEIKAAHAAEWKANTVAETFRTRRLSVIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEVEGEFRAHAAEWANTVAETFKETRRLSVIHDKLOAAATIRSM 349
QY 374 -SME-----RRRLGLDORAHSLDMLSP 394
Db 350 LSASLAGNHQELTFCMRTLNVHLTNERDLVLP 383

RESULT 11

US-09-828-746-2
; Sequence 2, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2

Query Match 45.0%; Score 1242.5; DB 9; Length 411;
Best Local Similarity 63.5%; Pred. No. 1.4e-92;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
QY 17 AAPVCQPKSATNGOPPAPAPTPTPLRSLSSRATVVA-RMEGTSQGLQTVWKKTVVAI 75
Db 2 RAPDLDPKSA-----AONSKPRLSPSTKPTVLASRVESDT---TINVMKWKTVSTI 50
QY 76 FVVVVVLTGVLFPALQEPFESSQKNTTALAEFLRDHVCVSPQELTILQHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKTFISQHSVCNSTELDELIIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHDGLSAPFPAGTVTTTIGYGNIAPISTETILFAGCIVFTTIPAVIF 195
Db 111 NAGIIPLGNTSNOISHDGLSSFPFAGTVTTTIGFNGISPRTEGGKIFCIIYALLGIPLF 170
QY 196 GFLLAGIGDQGTIFGKGIARVEDTFKWNVSQTKIRIISTITIFILAGCIVFTTIPAVIF 255
Db 171 GFLLAGVGDQGTIFGKGIARVEDTFKWNVSQTKIRIISTITIFILFGCVLFPALPAVIF 230
QY 256 KYIEGWTALSIYFVVVTLTTVGFGDFVAGGNAGINREWKYPLVWFWLVLGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDYFYPVWFWLVLGLAYFAAVL 289
QY 316 SMIGDMLRVLSKTKKEVEGEIKAAHAAEWKANTVAETFRTRRLSVIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEVEGEFRAHAAEWANTVAETFKETRRLSVIHDKLOAAATIRSM 346
QY 376 ERRRLGLDORAHSLDMLSPKRSV 399
Db 347 -KRKLSAELAGNHQELTFCMRTL 369

RESULT 12

US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 411
TYPE: PRT
ORGANISM: H. sapiens
US-10-121-746-83

Query Match 45.0%; Score 1242.5; DB 14; Length 411;
Best Local Similarity 63.5%; Pred. No. 1.4e-92;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNATNGQPAPAPPTPRLSISSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
Db 2 AAPDLLDPKSA-----AQNSKPRLSFSTKPTVLASRVESDT---TINVMKKTSTI 50
QY 76 FVVVVVYLTGGLVFPALQEPSSQKNTIALEKAEFLRDHVCVSPQLETLIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCVNSTELDELIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTIGYGNIASTEGGKIFCIIYALGIPLF 195
Db 111 NAGIPLGNISNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALGIPLF 170
QY 196 GFLLAGIGDQGTIFGKSIARVEKVFKEQVSTQKIRIVSTIFILAGCIVFVTPAVIF 255
Db 171 GFLLAGVGDQGTIFGKGIKVEDTFIKWVSTQKIRIISTIFILFGCVLFVALPAIIF 230
QY 256 KIEGWTALESYFVVVITTTVGDFVAGNAGINREWYKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGWSALDAIYFVVITTTTIGFDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289
QY 316 SMIGDLRLVLSKTKKEEVEGEIKAHAAEWKANTVABPRETRRLSVEIHDKLOAAITRSM 375
Db 290 SMIGDLRLVLSKTKKEEVEGEFPAHAAEWNTVABFEKTRRLSVEIYDKFORATSI--- 346
QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
Db 347 -KRKLSAELAGNHQELTFCRRTL 369

RESULT 13
US-10-745-210-2
Sequence 2, Application US/10745210
Publication No. US20040143855A1
GENERAL INFORMATION:
APPLICANT: TONONI, Giulio
APPLICANT: CIRELLI, Chiara
TITLE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
FILE REFERENCE: 054030-0044
CURRENT APPLICATION NUMBER: US/10/745,210
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/436,201
PRIOR FILING DATE: 2001-12-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-10-745-210-2

Query Match 45.0%; Score 1242.5; DB 16; Length 411;
Best Local Similarity 63.5%; Pred. No. 1.4e-92;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNATNGQPAPAPPTPRLSISSRATVVA-RMEGTSQGLQTVMKWKTVAI 75

Db 2 AAPDLLDPKSA-----AQNSKPRLSFSTKPTVLASRVESDT---TINVMKKTSTI 50
QY 76 FVVVVVYLTGGLVFPALQEPSSQKNTIALEKAEFLRDHVCVSPQLETLIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFISQHSVCVNSTELDELIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTIGYGNIASTEGGKIFCIIYALGIPLF 195
Db 111 NAGIPLGNISNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALGIPLF 170
QY 196 GFLLAGIGDQGTIFGKSIARVEKVFKEQVSTQKIRIVSTIFILAGCIVFVTPAVIF 255
Db 171 GFLLAGVGDQGTIFGKGIKVEDTFIKWVSTQKIRIISTIFILFGCVLFVALPAIIF 230
QY 256 KIEGWTALESYFVVVITTTVGDFVAGNAGINREWYKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGWSALDAIYFVVITTTTIGFDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289
QY 316 SMIGDLRLVLSKTKKEEVEGEIKAHAAEWKANTVABPRETRRLSVEIHDKLOAAITRSM 375
Db 290 SMIGDLRLVLSKTKKEEVEGEFPAHAAEWNTVABFEKTRRLSVEIYDKFORATSI--- 346
QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
Db 347 -KRKLSAELAGNHQELTFCRRTL 369

RESULT 14
US-09-939-484-8
Sequence 8, Application US/09939484
Patent No. US20020032322A1
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 1201-CIP-DIV-00
CURRENT APPLICATION NUMBER: US/09/939,484
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/144,914
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 08/749,816
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: FR 96/01565
PRIOR FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
ORGANISM: Murine
FEATURE:
OTHER INFORMATION: TREK-1
US-09-939-484-8

Query Match 44.9%; Score 1238.5; DB 9; Length 370;
Best Local Similarity 64.2%; Pred. No. 2.5e-92;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNATNGQPAPAPPTPRLSISSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
Db 2 AAPDLLDPKSA-----AQNSKPRLSFSTKPTVLASRVESDT---AINVMKKTSTI 50
QY 76 FVVVVVYLTGGLVFPALQEPSSQKNTIALEKAEFLRDHVCVSPQLETLIOHALDAD 135
Db 51 FLVVVLYLIIGATVFKALEQPHISQRTTIVIQKQTFIAQACVNSTELDELIQIVAAI 110
QY 136 NAGVSPIGNSSNNSSHWDLGSAFFPAGTIVTTIGYGNIASTEGGKIFCIIYALGIPLF 195

Db 111 NAGIIPLGSSNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLE 170
Qy 196 GFLLAGIGDOLGTIFGKSTARVEKVKQVSTKIRVISTILFILAGCIVFTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIF 230
Qy 256 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINREWKPLVWFWILVGLAYFAAVL 315
Db 231 KHIEGWSALDAIFYFVITLTTIGFGDYVAGG-SDIEYLDIFYKPVVFWILVGLAYFAAVL 289
Qy 316 SMIGDMLRVLSKTKKEEVEIKAHAAEWKANTAFRETRRLSVEIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEEVEIFRAHAAEWNTANTAFKETRRLSVEIYDKFORATSV--- 346
Qy 376 ERRRLGLDORAHSLDMLSPKES 398
Db 347 -KRKLSAELAGNHNOELTPCMRT 368

RESULT 15

US-09-939-483-8
; Sequence 8, Application US/09939483
; Patent No. US2002009458A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-939-483-8

Query Match 44.9%; Score 1238.5; DB 9; Length 370;
Best Local Similarity 64.2%; Pred. No. 2.5e-92;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;
Qy 17 AAAPVCPKSAATNGQPPAPPTPELSTSSRATVVA-RMEGTSQGLQTVNKKTKTVAI 75
Db 2 AAPDLDDPKSA-----AQNSKPLSFSSKPTVLASRVSDS---AINVMKTKVTSTI 50
Qy 76 FVVVVVYLVGTGLVFRALQPFESSQKNTIALEKAEFLRDHVCVSPQLETLIQHALDAD 135
Db 51 FLVVVLYLIIGAAVFKALQPOEISQRTTIVIQKTFIAQHACVNSTELDELIQIVRAI 110
Qy 136 NAGVSPIGNSSNNSHWDLGSAPFFAGTIVTTIGYNIAPSTEGGKIFCIYALGIPLE 195
Db 111 NAGIIPLGSSNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIYALLGIPLE 170
Qy 196 GFLLAGIGDOLGTIFGKSTARVEKVKQVSTKIRVISTILFILAGCIVFTIPAVIF 255
Db 171 GFLLAGVGDLGTIFGKIAKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIF 230
Qy 256 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINREWKPLVWFWILVGLAYFAAVL 315

Db 231 KHIEGWSALDAIFYFVITLTTIGFGDYVAGG-SDIEYLDIFYKPVVFWILVGLAYFAAVL 289
Qy 316 SMIGDMLRVLSKTKKEEVEIKAHAAEWKANTAFRETRRLSVEIHDKLOAAATIRSM 375
Db 290 SMIGDMLRVLSKTKKEEVEIFRAHAAEWNTANTAFKETRRLSVEIYDKFORATSV--- 346
Qy 376 ERRRLGLDORAHSLDMLSPKES 398
Db 347 -KRKLSAELAGNHNOELTPCMRT 368

Search completed: April 28, 2005, 13:41:12
Job time : 136 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:22:27 ; Search time 42 Seconds
(without alignments)
1232.491 Million cell updates/sec

Title: US-09-892-360-2
Perfect score: 2760
Sequence: 1 MFPLYTDFLSLVAVPAAAP.....IPTDTKOREPNNLSLEDRN 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	403	14.6	336	2 S65566	inward rectifier p
2	329	11.9	330	2 JC7703	TASK-5 protein - h
3	326	11.8	1001	2 T13807	potassium channel
4	315.5	11.4	329	2 T43509	probable potassium
5	307	11.1	336	2 T32347	outward rectifier
6	300.5	10.9	364	2 T43361	probable potassium
7	298.5	10.8	393	2 T25392	hypothetical prote
8	298.5	10.8	1910	2 H88124	protein t12C9_3 [i
9	290.5	10.5	334	2 T19860	hypothetical prote
10	282.5	10.2	392	2 T45032	hypothetical prote
11	268.5	9.7	522	2 T42865	hypothetical prote
12	265.5	9.6	522	2 T21834	hypothetical prote
13	264.5	9.6	444	2 T26229	hypothetical prote
14	264	9.6	551	2 T16426	hypothetical prote
15	262.5	9.6	555	2 T43357	potassium channel
16	262.5	9.5	443	2 T21598	hypothetical prote
17	260.	9.4	461	2 T43394	potassium channel
18	258.5	9.4	513	2 T28933	hypothetical prote
19	255	9.2	452	2 T21118	hypothetical prote
20	252.5	9.1	586	2 T21683	hypothetical prote
21	248	9.0	325	2 T15584	hypothetical prote
22	247	8.9	427	2 T27681	hypothetical prote
23	245	8.9	1136	2 T26953	hypothetical prote
24	244	8.8	504	2 T22269	hypothetical prote
25	233.5	8.5	484	2 T43529	probable potassium
26	233.5	8.5	519	2 T16629	hypothetical prote
27	233.5	8.5	1539	2 T30037	hypothetical prote
28	229.5	8.3	383	2 T23182	hypothetical prote
29	227.5	8.2	307	2 H89074	protein twk-24 [im

hypothetical prote
hypothetical prote
hypothetical prote
f22b7.7 protein -
outward-rectifier
potassium channel
hypothetical prote
probable potassium
potassium channel
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65566
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, EMO J. 15, 1004-1011, 1996
A>Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel A:Reference number: S65566; MUID:96183184; PMID:8605869
A:Accession: S65566
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: UNIPROT:O00180; EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g1086490

Query Match 14.6%; Score 403; DB 2; Length 336;
Best Local Similarity 33.2%; Pred. No. 2e-20;
Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;

Qy 76 FVVV-VVYLVGSLVFRALQEPFESSQKNTALEKAEFLRDHVCVSPQELTFLQHALD 133
Db 25 FLVLGYLLYVFGAVFSSVELPYEDLLRQLRKLKRFLSEHECLSSQQLQPLGRVLE 84
Qy 134 ADNAGVSPIGNSSNNSSHWDLGSAFFAGTITVITIGYNIAPSTEGGKIFCLLYAIFGIP 193
Db 85 ASNYGVSVLGNASGN-WNWDFTSALFFASTVLTGTGYHTVPLSDGGRKAFCLLYSVIGIP 143
Qy 194 LFGFLLAGIGDQLGTIFGKSTARVEKVRKKQV-----SQTKIRVISTIL--FILA 242
Db 144 FTLLFLTAV-----VQRTVTVTRPVLYFHIRWGFQKQVAVIHAVALGFTVV 192
Qy 243 GCIVFVTIPAVIFKYIE-GWTALESIIYFVVVLTGFGDFVAGNAGINRYEWYKPLVW 301
Db 193 SCPPF--IPAAVFSVLEDDNNFLSFYCFISLTIGLDVVPBGYNQKRELKYGIT 250
Qy 302 FWILVGLAYFAVLISMGLMRLVLSK-----KTEEVGEIKAAHAE 342
Db 251 CYLLGLLIAMLVLETFCR-LHELKFRKRMFYVKKDKEDQVHIIE 295

RESULT 2

JC7703
TASK-5 protein - human
C:Species: Homo sapiens (man)
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: JC7703
R:Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A>Title: TASK-5, a new member of the tandem-pore K+ channel family.
A:Reference number: JC7703; MUID:21303050; PMID:11409881
A:Accession: JC7703

A:Molecule type: DNA
A:Residues: 1-330 <KIM>
A:Cross-references: GB:AL118522
C:Comment: This protein, a new member of the tandem-pore K⁺ channel family with four transmembrane domains, is secreted by the cell and does not produce a functional plasma membrane K⁺ current by itself.
C:Genetics:
A:Gene: task-5
A:Map position: 20q12
C:Keywords: transmembrane protein
P:7-30/Domain: transmembrane segment #status predicted <TMS1>
P:107-128/Domain: transmembrane segment #status predicted <TMS2>
P:129-155/Region: hydrophobic cytoplasmic linker #status predicted
P:156-180/Domain: transmembrane segment #status predicted <TMS3>
P:220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match 11.9%; Score 329; DB 2; Length 330;
Best Local Similarity 32.4%; Pred. No. 2.6e-15;
Matches 85; Conservative 46; Mismatches 97; Indels 34; Gaps 9;

QY 75 IFVVVVVYLVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSELTLIQHALDA 134
DB 11 LVLTCTCLLVGAADFALSAEASGRQR-LLVQKRGALRRKFGFSAEDYRELRLALQA 69
QY 135 D--NAGVSPIGNSSNNSHDGLSAPFAGTIVTTIGYGNAPSTEGGKIFCILVAIFGI 192
DB 70 EPHRAG-----RQMKPGSGFYFAITVTTIGYGHAAAGTDSGKVFVALLGI 118
QY 193 PLFGLLAGIGDGLTIFGKSTARVEKVRKKQVSTQKIRVISTILFILAG--CIVFVT 249
DB 119 PLTVTFOSLGERLNAV-----VRLI--LLAAKCGILRWTCVSTENLVVAGLACAATIA 172
QY 250 IPAVIFKIEGTALLESIFVVTTLTTVGGDFVA--GGNAGINRYREWYKPLVFWFVLVG 307
DB 173 LGAVAFSHFEGWTFPHAYYCFITLTTIGFGDFVALQGEA-LQRKLPVAFSFLYLLG 231
QY 308 LAYFAAVLSMI-----GDW 321
DB 232 LTVIGAFNLVVLFLVASADW 253

RESULT 3
T13807
potassium channel protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13807
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from *Drosophila*
A:Reference number: Z17770; MUID:97075152; PMID:8917578
A:Accession: T13807
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1001 <GOL>
A:Cross-references: UNIPROT:Q94526; EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC692
C:Genetics:
A:Gene: ORK1
A:Cross-references: FlyBase:FBgn0017561
A:Map position: 1

Query Match 11.8%; Score 326; DB 2; Length 1001;
Best Local Similarity 22.9%; Pred. No. 1.8e-14;
Matches 123; Conservative 93; Mismatches 193; Indels 128; Gaps 20;

QY 68 KKTVAIVVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSELT 127
DB 5 RW---ILLIFIVISYLMFGAAIYTHIEGEEK-----ISRAQRKAQIAINEYLLEL 54
QY 128 -----IQHALDADNAGVSPIGNSSNNSHDGLSAPFAGTIVTTIGYGNAPSTEGGKIFCI 176
DB 55 GKNTTQDEILQRIIDYCDKPVLPPTDYDDTPYTWTFHAFHFAFTVCSTVGYGNIST 114
QY 177 TEGGKIFCILYAFIGLPLFGLLAGIGDGLTIFGKSTARVEKVRKKQVS-----QTK 230

DB 115 TFAGRMIMIAYSVIGIPVNGILFAGLGE-----YFGRTPEAIYRYRYKCYKMSDTHYVPPQ 170
QY 231 IRVISTILFL-ILACGIVFVTPAVIFKYIEGTALLESIFVVTTLTTVGGDFVA--GGN 287
DB 171 LGLITTVIAIPGIALPGLFLPSVWVTFYFENWPYSISLIYVYVTTTIGFGDVFPTFGAN 230
QY 288 AGINRYEW---YKPLVFWFVLVGLYFAAVLSMIGDMLRVLSKK-----TKEEVGSIKAHA 340
DB 231 QPKFEGGWVYVQIFVFWFISGLYLVIMTFTIRGLQ--SKKLAYLEQQLSNKLATQ 288
QY 341 AEWKANVTAEFRFRRLS-----VEIHDKLQRAATIRSMERRR-----LGL 382
DB 289 NRIWSGVTQKGVYLRRLMNELYILKVPYVYTDVIAITLPRSNSCPDLSMYRVEPAPIS 348
QY 383 DORASL--DMLSPEKRS--VFAALDTGRFKASSQESINNRP-----NNLRL 425
DB 349 RKRAFSCADNVAAQREAGVHANSDELTKLDRKTFETAEAYRQTDTLLAKVVALAT 408
QY 426 KGP-----EQLNKHG--QGASEDNI-----INFGSTSRLLTKRKNKOLKTLPE-- 467
DB 409 VKPPPAEQEDAALYGVYHGFSDSOLASEWSFSTWNEPTSPRRPRARACSDPNLEAPRWQ 468
QY 468 -----DVQKIYKTFRN-----YSLDEKKEEETEK 492
DB 469 SERPLRSHNEWTSGDNQIQEAFNQRYKQQRANGAANSTMVHLBPDALBEOLEK 525

RESULT 4
T43509
probable potassium channel chain n2P38 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43509
R:Wang, Z.W.; Salter, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in *C. elegans*.
A:Reference number: Z22450
A:Accession: T43509
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-329 <WAN>
A:Cross-references: UNIPROT:O17185; EMBL:AF083652; PIDN:AAC32863.1

Query Match 11.4%; Score 315.5; DB 2; Length 329;
Best Local Similarity 31.6%; Pred. No. 2.2e-14;
Matches 86; Conservative 48; Mismatches 99; Indels 39; Gaps 9;

QY 73 VAIFVVVVVYLVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSELT 127
DB 9 LSLIVCTLTLLVGAADFALSAEASGRQR-LLVQKRGALRRKFGFSAEDYRELRLALQA 67
QY 128 --IQHALDADNAGVSPIGNSSNNSHDGLSAPFAGTIVTTIGYGNAPSTEGGKIFCI 185
DB 68 KSVPH-----KAGY-----QWKPGAFYFAITVTTIGYGHSTPMTDAGKVF 111
QY 186 LVAFIGLPLFGLLAGIGDGLTIFGKSTARVEKVRKKQVSTQKIRVISTILFIL-- 241
DB 112 LYALAGIPLGLIMFQSIGERWNTFAKLLRIRRAAGKQPI-----VTSSDLIFCTGW 165
QY 242 AGCIVFVTPAVIFKYIEGTALLESIFVVTTLTTVGGDFVAGNAG-INRYEWYKPLV 300
DB 166 GGLLIFG--GAFMFSSYENWTYFDAVYCYFVTLTTIGFGDYVALQKRGSLQOPEYVPS 223
QY 301 WFWILVGLYFAAVLSMIGDMLRVLSKKTKEE 332
DB 224 LVFILFGLTIVISAANLL--VLRFLTMNTEDE 253

RESULT 5
T32347
outward rectifier potassium channel homolog twk-23 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C; Accession: T32347
R; Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of *C. elegans* cosmid F34D6.
A; Reference number: Z21153
A; Accession: T32347
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-336 <MUR>
A; Cross-references: EMILPROT:O17185; EMBL:AF025454; PIDN:AACT1151.1; GSPDB:GN00020; CESP:
A; Experimental source: strain Bristol N2; clone F34D6
C; Genetics:
A; Gene: twk-23; CESP:F34D6.3
A; Map position: 2
A; Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match	11.1%;	Score 307;	DB 2;	Length 336;
Best Local Similarity	30.3%;	Pred. No. 8.8e-14;		
Matches	84;	Conservative 50;	Mismatches 101;	Indels 42; Gaps 9

QY	73	VALFVVVVVVLVTGGLVPRALEQPPESQKTIALEKAEPLRDHVCTVPSQSLFTLIQHAL	132
DB	9	LSLIVCTLTLLVGAADFALETENEILQVRGLG-----EPRKLIVORREKL	55
QY	133	-----DADNAG-----VSPIGNSSNNSSHWDLGSAFFFACTVTTTIGYGNIASTEGG	180
DB	56	KTKNNMGNADYEILEATIVKSPHKA--GYQWKPFGAIFYATTVTTIGYGHSTPMTDAG	113
QY	181	KIFCLYAIAPGIPLPFGLLAGIGPOLGTIFGKSIARVEKVRKKQVSQTKIRVLTSLFI	240
DB	114	KVFCMLYALAGIPGLIMFQSIGERMNTFAAKLIRFIRRAKGQPI-----VTSSDLII	167
QY	241	L-----AGCIVFVTLIPAVIFKYIEGWTALESIFYVVVLTTLTVPGDFVAGGNAG--INTRYE	295
DB	168	FCFGWGGLLIFF--GAFMFFSYENWTVFDVAVYCFVTLTTTIGDFGYVALQKRGSLQTPQ	225
QY	296	YKPLVFWFIIIVGLYAFPAAVLSMIGDWLRVLSKTKBE	332
DB	226	YVPFSLVFIIFGLTVISAAAMNLL--VLRFLTWTNTEDE	260

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RESULT 6
T43361
probable potassium channel chain n2P20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43361
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43361
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-364 <WAN>
A:Cross-references: UNIPROT.O76790; EMBL.AF083646; PDB:AAIC32857.1

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	Query Match	10.9%;	Score 300.5;	DB 2;	Length 364;	
	Best Local Similarity	26.8%;	Pred. No. 2.8e-13;			
	Matches	106;	Conservative	78;	Mismatches 124;	Indels 87; Gaps 19;
Qy	70 KTVVAIFVVV--VVYLVTGVLGFALQPESPSSOKNTIALEKAFSLRDHV-----CVSPQE	123	:	:	:	:
Dd	7 KSARALLILSTFTYLLFGAVVPDKLSE----SEKOTWVRDEIRITRLRKHKNFNSERD	61	:	:	:	:
Qy	124 LETLIQHLDADNAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYCNIAPIAPTEGGKIF	183	:	:	:	:
Dd	62 L-----HLPEA--IAIKSIQQA--GYQMWFAGAFYFATVITTVGVGHSPASPTNAGKL	112	:	:	:	:
Qy	184 CIIYAIFGIPLPGFLIAGIDQLGTIFGKSJARVEKVFRK-----KQVSOTKIRVIS-T	236	:	:	:	:
Dd	113 CMIFALFGVMGLIMFOISICERNVNTFYAISLRKPSDSLHOOGFTCLQOEVTTHLLMYSLT	172	:	:	:	:

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237 QY ILF--ILAGCIVFTIPAVIFKVEGWTALESIYVVVTLTVTGFGDFVAGGNAGINyre 294
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
173 Db IGFVWIVSGTYMETH-----IEKWSIDDAYVFCMTPTSTIGFGDLVP--LQOVNALQ 222
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
295 QY WYKPLWF---WLVCLAYFAAVLSMIGDWLRVLVKTKKEVGCEIKAAAEKVAATAE 350
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
223 Db -DQPLVFYFATIFILIGLAVFSACVNLL-----VLGFMASNADE----VTAA 264
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
351 QY FRE-----TRRLSVSEIHDKLQRAATIRSMERRRLGLDORAHSLDMLS----- 393
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
265 Db QREPPSAIVLERFRNSLDVSQIFNIKHSTGVLP-----GRPRMYSIVENSTADVHLR 320
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
394 QY --PEKRSVFAALDTGRFKASSQE---SINNRPNNL 423
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
321 Db RRSTRSIQTVCGCCKPAPRRHRFSLTRPTNI 355
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 7
T25392
hypothetical protein T29A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25392
R;flvda C
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submitted to the EMBL Data Library, March 1997
A;Reference number: Z20027
A;Accession: T25392
A;Status: preliminary; translated from GR/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-393 <WIL>
A;Cross-references: UNIPROT:Q9XU07; EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00002
A;Experimental source: clone T28A8
C;Genetics:
A;Gene: CESP:T28A8.1
A;Map position: 3
A;Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match	10.8%	Score	298.5	DB 2	Length	393			
Best Local Similarity	27.1%	Pred. NO.	4.2e-13						
Matches	85	Conservative	50	Mismatches	94	Indels	85	Gaps	11

Qy	69	WKTIV-----VAIFVVVVVYLVTGGLVFRALPQPSSQKNTALEKAFLRDHVCVSP	121
Db	4	WKTIVARIILAHVLSLVSVYVGFAGFLFYQLEQ-----NEVEVRARNIERFI	53
Qy	122	QBLETLIQIALDADNAGVSP-----IG-----NSSNNS	149
Db	54	-HKRQMIHLNWMRESGIGHVVEDLAVKYDVNTRILFEAPDTHCIGAKHLRPGGDE	112
Qy	150	SHWDLGSAFFAGTVTTTIGYGNIAPISTGGKIFCILYAI FGIFLFGFLAGIGDQLGTI	209
Db	113	YNWYMTALPFTTLLTTTIGYGNLTPTVTRGKGLCILYALFGVPL---ILITVAD-IGKF	168
Qy	210	FGKSIARVEKVRK--KQVSTQKIRVIST-----ILFILAGCI	245
Db	169	LSENIVOLITWYRKURKBEKSKQKYSVISSKODRKNKBDLNLDLHLENYISIPILVAILL	228
Qy	246	VFTTIPAVIFKYTEGTALTESIFVWVTLTTTGVGDFVAGGNAGINRYEWKPLVWFWIL	305
Db	229	SVITFGAVLSMWEGWDFFSGFFSPITWTVGFGDIVP-----LKREYY-ILDLCYII	281
Qy	306	VGLAYFAAVLSMIG	319
Db	282	IGLSITTMCIDLVG	295

RESULT 8
H88124
protein T12C9.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001
C;Accession: H88124

R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: AY5000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H89124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <STO>
A:Cross-references: GB:chr_II; PIDN:AC7L1141.1; PID:gl086770; GSPDB:GN00020; CESP:T12C9.3
A>Note: proline-rich
C:Genetics:
A:Gene: T12C9.3
A:Map position: 2

Query Match 10.8%; Score 298.5; DB 2; Length 1910;
Best Local Similarity 21.2%; Pred. No. 3.3e-12;
Matches 121; Conservative 90; Mismatches 197; Indels 163; Gaps 22;
QY 10 LSLVAPPAAPVCPKSAATNGOPAP-APT-TPRLSSRAATVVARMEGTSQGLQT 65
DB 134 LSFSTPATRKACLEKQV---HPPIHETPPQFRRFSIFGLLESARPDDETTTLQN 190
QY 66 VMKWTV---VAIFVVVVVLTGGLVFRALFQPFESSQK---NTIALEKA----- 110
DB 191 IRKYAKLALPHIVLVVCIVATIGAWIFYTLESFNEDELKTKETGRKTIAMESNLIYKIN 250
QY 111 -----EFLRDHVCVSOEL-----EYLIOHA-----LDADNAGVSPGN 144
DB 251 NNEKEVWKEDIEKELMLYSEKLYKAFKQYVRYSDVRTTIGFGRSSYEADETG---GD 306
QY 145 SNNSSH-----NDLGSARFFAGVITVIGYGNIAPESTGGKIFCILYALF 190
DB 307 SERKRHRHGNKRGDSGEMKMTSSALFPAAITWATIGVNIIVPTPLGRACVLPALF 366
QY 191 GIPFLFGLAGIDQAG--TIF-----GKSIARVEKVRK----- 223
DB 367 GAPIAITIGDLGKFLSECTWLYKHMKGSRALDSAMKFRGLEDSISDDLESANQD 426
QY 224 -----KQVSTKIRVISTILFILAGCIVFTTIPAVIFKTEGWTALESYFVVVILT 275
DB 427 SSILDMWDEIDKSEVPVLMFTIIL---LYTAFGGILFLEDSYNDAPFYFISLT 482
QY 276 TVGFGDFVAGGNAGINREWRKPLVFWLVLGLVAPAAVLSMIG----- 319
DB 483 TIGFGDIVPENHD-----YTAIMLIYLGVLGVSVTTCIDLAGIQYIKIHFGRKFG 535
QY 320 -DMLRVLSKTK-----EEVGEIKAHAAEMKANYTABFRETRRLSVIHDKLQR 368
DB 536 TDLQVLYKKRMLERLANGQGEIILRYVHAVE-----KFEREQEQLOQKMBEEDPP 588
QY 369 AATIRSMERRRGLDQRAHSL-----DMLSPKRSV---FAALTGRPKASSQES 415
DB 589 SIESKGFDSMMRIDDLSAFQLRFYDITYDEEDLFSFTIHSVRSFQPSVMSHSSARSQS 648
QY 416 I---NNRPNNRLKGPQLNKHQGASEDNI 443
DB 649 CRPQRNGASWDESGP-SUSEHCSLSTEPSV 678

RESULT 9
T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19860
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19860
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 10.5%; Score 290.5; DB 2; Length 334;
Best Local Similarity 28.6%; Pred. No. 1.2e-12;
Matches 89; Conservative 67; Mismatches 94; Indels 61; Gaps 15;
QY 70 KTVVAIFVVV---VVLVTGGLVFRALFQPFESSQKNTIALEKAEPLRDHV---CVSPQES 123
DB 7 KSARALLILSTFTVTLFGAMVFDKLE-----SEKDTWVRDEIRITDLRKHKYNFSEED 61
QY 124 LETLIOHALDADNAGVSPIGNSSNNSHWDLGSAFFRAGTIVTTTGYGNIAPSTGGKIF 183
DB 62 L-----HLFEA---TAIKSIPQOA---GYQWQFAGAPYFATVTVTTVGYGHSAPSTWAGKLF 112
QY 184 CILVAIFGIFLFGFLLAGIGDQAGTIFGKSIARVEKVRK-----KQVSTKIRVIS--T 236
DB 113 CMIFALGFVFMGLFMFQSIGERVNTFIAYSLHKFRDSLHQOQFTCLQEVTPHLLMVSIT 172
QY 237 ILF--ILAGCIVFTTIPAVIFKTEGWTALESYFVVVLTITVVGDFVAGNAGINVRB 294
DB 173 IGFVIVSGTYMFT-----IEKWSIFDAYYFCMITFTSTIGFGLVP---LQOVNALQ 222
QY 295 WYKPLVWF-----WILVGLAYFAANVLMTGMDWLVLSKTKSEVGEIKAHAAEMKANYTAE 350
DB 223 -DQPLVFEATTMFLIGLAVSACVNL-----VLGFMASNADE-----VTAA 264
QY 351 FRETRRRLSVE 361
DB 265 QREPPSAIVLE 275

RESULT 10
T45032
hypothetical protein Y39B6.f [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45032
R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berke, M.; Bonfield, J.; Burton, R.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifkin, L.; Roopra, A.; Saunders, D.; Nature 368, 32-38, 1994
A:Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonhammer, S.; tock, L.; Wilkinson-Sproat, J.; Wohlman, P.
A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A:Reference number: S43531; MUID:94150718; PMID:7906398
A:Accession: T45032
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-392 <WIL>
A:Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446
A:Experimental source: clone Y39B6B
C:Genetics:
A:Map position: 3
A:Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
A>Note: Y39B6.f

Query Match 10.2%; Score 282.5; DB 2; Length 392;
Best Local Similarity 31.7%; Pred. No. 5.3e-12;
Matches 77; Conservative 46; Mismatches 97; Indels 23; Gaps 8;
QY 90 FRALFQPFESSQKNTIALEKAEFLRDHVC---VSPQELTIOHALDADNAGVSPIGNSS 146
DB 118 FSRIEVPLEKIEREAY-LDYQNWDRDLIQIDSEIDKLF---LNIREAALNGIWMDR 173
QY 147 NNSS---HWDLGSAFFAGTIVTTTGYGNIAPSTGGKIFCILYALFGLFPELLAGIGD 204
DB 174 NLTSDPNWTFQAFAGTISTVGYGRVSPRTEYKLFILYCVIGIPLTLLALLSAIVA 233

QY 205 QL-----GTIFGKSIAARVKKVQKQVSTKIRVI--STILFILAGCIVFVTPAVIFKVI 258
DB 234 RMREPSHKLRLGLNORGLHLFTVNHQLIHVGVPASLLLFVFA-----IPAWVFSS 286
QY 259 B-GWTALESIIYFVVVTLTTVGGDFVAGGAGNINREWKPLVFWILVGLYFAVAVLSM 317
DB 287 ETDWSLYDAFYCYFVSLTTIGLDFPDPGDDPNQSGRLYKIGATVYLMGGLCQMLFLAT 346
QY 318 IGD 320
DB 347 LYD 349

RESULT 11
T24265
hypothetical protein T01B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24265
R:Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19866
A:Accession: T24265
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-522 <WIL>
A:Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4
A:Experimental source: clone T01B4
C:Genetics:
A:Gene: CESP:T01B4.1
A:Map position: X
A:Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 9.7%; Score 268.5; DB 2; Length 522;
Best Local Similarity 22.3%; Pred. No. 7.2e-11;
Matches 120; Conservative 89; Mismatches 181; Indels 147; Gaps 21;

QY 73 VAIFVVVVVYLVGTGLVFRALF---QPPE-----SSQKNTIALEKAEFLRDHVCVSP 121
DB 39 IMLIILILGACLGGMFQALBYDQOQLEAEKRVLSSESLLAVNLEHLKQVNCQS 98
QY 122 QB-----LETLIQHALDADNAGVSPICGNSNNSHWDLSGAPFAGTIVTIGYGNIA 174
DB 99 NEKRCLELITKTFIORSDEEGEG-----WRWDFWNSVFSATIPTTIGYGNLA 147
QY 175 PSTEGGKIFCIYALFGLPLGFLAGIDQGLTIFGKSI-----ARVEKVRKQVQSQT 229
DB 148 CKNLGRITATIIYGMIGIPLMLFVLNFG-ELCVKWKAKIQPNVQOCLKCKCFGRKQKAS 206
QY 230 KIRVIST-----ILPLAGCIVFVTPAVIPKVIKGTALBSIY 268
DB 207 SLASITKEMLEVPEVEDDKEDTTFQLRWGLLVILFVLCSFVSVFWENWDFLTAFY 266
QY 269 FVVTLTTVGGDFVAGGAGNINREWKPLVFWIL--VGLAYPAAVLSMIGD----- 320
DB 267 PFPVSLSTIGFDIVP-----DHPTACALFVLYFGLALFAMVYAILQEVENQY 317
QY 321 -W-LRVLSKTKYEEVEIKAAHAWEKA---NVTAEFRTRRLSVIEHDKLQRAATIRSM 375
DB 318 MWALELDQYOEKLKODMYDEDEKADKNDMHFSKKEPVRGPRILLQD-LLRGPDALKIS 376
QY 376 ERLRLGIDQRAHSLDMLSPKRSVPAALDTGRFKASSQESINNRPNRLKGP-EQLNKH 434
DB 377 GGRSSSD--ASSVITEASDE-----DTRHFKV-----GRAILAEAPADERASNH 420
QY 435 GQASDENIINKFGSTSLTRKKNKDLKTLPEDEVQKIYKTFR-----NYSLDEEK 485
DB 421 GTQLNSCTVSNHSDC-----QIEAIVFSFHFISFINQFNYSDESGL 463
QY 486 KEETERKCNLS-----DNSSTAM-----LTDCTQQAHLENG 517
DB 464 EEHQLEYDNTSGTPPPYGDPTFTTNFQTRDETIVSLAEKTPLSLKNKVLKEENEDENG 520

RESULT 12

T21834

hypothetical protein F36A2.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21834

R:Lennard, N.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19476

A:Accession: T21834

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-528 <WIL>

A:Cross-references: UNIPROT:P90863; EMBL:Z81077; PIDN:CAB03071.1; GSPDB:GN00019; CESP:1

A:Experimental source: clone F36A2

C:Genetics:

A:Gene: CESP:F36A2.4

A:Map position: 1

A:Introns: 45/3; 81/3; 114/3; 151/3; 195/1; 306/1; 326/1; 368/2; 413/1; 464/2; 494/1

Query Match 9.6%; Score 265.5; DB 2; Length 528;

Best Local Similarity 22.2%; Pred. No. 1.2e-10;

Matches 122; Conservative 86; Mismatches 163; Indels 179; Gaps 26;

QY 79 VVYLVTCGLVFRALF-----QPPE-----SSQKNTIALEKA 110

DB 25 VLYIILGAIIVFQMLEGHLNDFSNPKHFGPKVQDKFFETIFRRWSKGAN---FKKS 81

QY 111 EFLRDHVCVSPQ-----ELETILI-----QHALDADNAGVSP 142

DB 82 ALKQDHMAKIQNAKYDYDKLWSVAKRDRDKYKVNVEDLIKVKEDTDDFNDYDVTVFYA 141

QY 143 -----GNSSNNSHWDLSGAPFAGTIVTIGYGNIAPISTEGGKIFCIYALFGLPFGF 197

DB 142 HRAVRHGYDESDPTWDPANSVFTTTMLTISIGYGVAPSTFGRLFGVYICIGIPLTLV 201

QY 198 LLAGIGDGLG-TIP-----GKSIARVEKVRKQVQSQ-----TKIR 232

DB 202 TVANVAKPLSETIFPLHYELWNKLEWKRK--RKEGEVADPLQPMFGDDENESEILDRVR 259

QY 233 VIS-----TILFILAGCIVFVTPAVIPKVIKGTALBSIYFVVVTLTTVGGDF--VAGN 287

DB 260 LVREPLTVFPFV--FVYGCIAWVRYWTVTWVTSYLYFIFISILTVGGDIRPSPGN 316

QY 288 AGINREWKYKPLVWF--WILVGLAYPAAVLSMIGD-----LRVLSKTKYEE---VGE 335

DB 317 -----IWTLLAFVVVGVILTTMCMDVVGRMYLKEIHYLGRKLKSSNPFPYLLRE 364

QY 336 IKAAHAWEKANVTAEFRTRRLSV-----EIHDKLQRAATIRSMERRRL 380

DB 365 AKAR-----RRAAMASLLAQALAKGMIFAHKDYNELARKKSKRKEKR- 408

QY 381 GLDQRAHSLDMLSPKRSVPAALDTGRFKASSQESINNRPNRLKGP-EQLNKHQCGASE 440

DB 409 -----GSHVL-----PNEKFMFARLPD--PPSDCQVSTSAVSVRLWAPPF-----SP 451

QY 441 D-----NIINKFGSTSLTRKKNKDLKTLPEDEVQKIYKTFRNYSLDEKKEEETKMC- 494

DB 452 DPDLTYNIRYRLNATAVFKDQQRSLRALKFIKTDKI--EFHKCVGHSGKSTIDVWDSICE 509

QY 495 NSDMSSTAML 504

DB 510 KEDNETTALL 519

RESULT 13

T26229

hypothetical protein W06D12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26229

```
A;Map position: X  
A;introns: 14/3; 65/3; 95/2; 118/1; 165/3; 267/1; 297/2; 334/3; 385/2; 477/1; 513/2;  
  
Query Match          9.6%; Score 264; DB 2; Length 551;  
Best Local Similarity 20.3%; Pred. No. 1.6e-10;  
Matches 108; Conservative    94; Mismatches 205; Indels   124; Gaps   16;  
  
Qy      74 AIFVVVVLVTGLVFRALESQPFESSOKNTALEKAEFLRDHVCVSPOELEYL----- 127  
        :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db       24 SLLMLVLLYPLGGGFIDRIETNAHAEMK-----RNERINRTACVS-QILHSIRWSHN 76  
        :::::::::::::  
  
Qy     128 ----IQHALDADNAGVSPIGNSNNSSHWDLGSAFFPACTGVIITTCGYGNIASTEGGIKF 183  
         |::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
```

QY	184	CILYALFIGPLGFLLAGIQDGLGTTIPGKSIARVEKVRKQVSGTKI-----RVIS	235
Db	133	CIVYGICGIPVMTIIIANVGOYLNNPAGDSRRKIEAYRQORRMSKASLAGIKYKESSIQV	192
QY	236	TIILFILAGCIVFTIIPAVIEKYIEG-WTALESYIFVVVLTITVTCFGDFVAGNAGINVRE	294
Db	193	TSJALLCVFIYVAVGALLPLNGELDFNGLYFNFLCLTAIDFGQLVP-----IRV	245
QY	295	WYKPLVWFNLIUGLA-----YFAAVLSIMGDMLR	323
Db	246	ELLPITFLYCYIGLAITTAINTGSEYMKLHYWGKMNAAQTRIFPGGKTLKVRDLHL	305
QY	324	VLSKKTKEVEGETKAHAEMKANVTAFRETRRRLSVEIHDKLQRAATIRSM-----	375
Db	306	AVGKKCVGFGMDALDLENVVERTIANQSGREP-PEDLNDEPPREPSRPIIHSPCSTR	364
QY	376	-----ERRRLGDQRAHSIDMLSPKRSVFAALDTGRFKASS	412
Db	365	PSNPPMSPSPREDHPPIFKMDAPAPRSLPLPAYELDI---KKPIQALLSNEPMQSA	420
QY	413	QESINNRPNNLRLK-GPEQLNKH-----GOGASEDNII---NKFGSTSRLTWR	456
Db	421	QEXLFDNDLTFQIEINTELVEDHKCBSSVIIIEPPATFEDMTIQLHSLCVEDYERBEKVPCR	480
QY	457	KNKDLKKTLPEDVQKIYKTRFNYSILDBEKEEETEKMCNSDNSSMTAMLTDC	507
Db	481	-FREKKEMYGRDPRKLYET---YQEBWDRLERLSDRKHGPPRKSVNLNLSNC	527

A;Accession: I13357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-555 <WAN>
A;Cross-references: UNIPROT:Q20673; EMBL:AF083645; PIDN:AAC32856.1

Query Match 9.6%; Score 264; DB 2; Length 555;
Best Local Similarity 20.3%; Pred. No. 1.6e-10;
Matches 108; Conservative 94; Mismatches 205; Indels 124; Gaps 16

Qy 74 AIFVVVVLVTGLVFRALEQPPESSQNTIALEKAEFLRDHVCVSQPLELTL----- 127
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 28 SLMLVLVLYSLGFGFIDRIETNAEAK-----RNERINRTACVS-QILHSIHRWSHN 80

Qy 128 -----IQHALADNAGVSPIGNSSNNSHWDLGSAPFFACTVITTCYGNIASTGGKF 183
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 81 QTHKVQVAEDIADE----FEPKDERSEWNFTVTLGYGVITTLGYNRIAPIYTGRMP 136

Qy 184 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSARVEKVPKKQVSOTKI-----RVIS 235

Db 137 CUVYICIGIPVTMIINWQYLNFPAGDSRRKIRAYQOORMSKASLAGKIYKESSIQV 196
Qy 236 TILFILAGCIVFTIPAVIFKYIEG-WTALESIIYFVVTLTTVGFQDFVAGGNAGINTYRE 294
Db 197 TSLALLCVFLIYVAVGALLPLLLNGELDPFNGLYFNFLCLTAIDFGQLVP-----IRV 249
Qy 295 WYKPLVWFILVGLA-----YFAVLUSMIGDWLR 323
Db 250 ELLPITFLYVCIGLAITTIAINIGSEYMKKLYHWGKKMKNAAQTRIFGGKTLKVRDLH 309
Qy 324 VLSKKTKEEVGRIKAHAAEWKANVTAEFRETERRLSVEIHDKLOAAATIRSM----- 375
Db 310 AVGKCGVEPGMIDLDLENVVERTIAMQEGREP-PEDLNDEPPRPSRSTIHSPCSTR 368
Qy 376 -----ERRRLGDORAHSLDMLSPEKKSVEFAALDTGRFKASS 412
Db 369 PSNPPMSPSPREDHPFIFKMDAPAPRSPPLPAYELDI-----KKPIFQALSNEPMQSA 424
Qy 413 QESINNRPNLRLK-GPQLNKH-----GQASBDNII-----NKFGSTSRLLTKR 456
Db 425 QEKLFDLDTTQIEINTELBVDHKCESVIIIEPPATFEDMTIQHSLCVEDYEREKVPKR 484
Qy 457 KNKOLKKTLPEDVQKIYKTFPNYSLDEKKGEETEKMCSNDSNSTAMLTDC 507
Db 485 -FREKKEMYGRDPKLYET---YQBEWDRLERLSDRKHGPRRKSVINLSNC 531

Search completed: April 28, 2005, 13:26:02
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 13:22:27 ; Search time 180 seconds
(without alignments)
1530.548 Million cell updates/sec

Title: US-09-892-360-2
Perfect score: 2760
Sequence: 1 MFELYTDFFLSLVAVPAAP.....IPTDTKREPNNLSLEDRN 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2760	100.0	538	1	C1WA_HUMAN
2	2697	97.7	543	1	Q6B014
3	2584.5	93.6	538	2	Q60834
4	2578.5	93.4	535	2	Q8BUW1
5	2560.5	92.8	538	1	C1WA_RAT
6	2180.5	79.0	453	2	Q8B2B0
7	2117	76.7	546	2	Q68EY1
8	1251.5	45.3	411	1	C1W2_MOUSE
9	1251.5	45.3	414	2	Q6P6P9
10	1247.5	45.2	426	2	Q920B6
11	1244.5	45.1	411	2	Q8HY88
12	1242.5	45.0	411	2	Q9NRT2
13	1218.5	44.1	426	1	C1W2_HUMAN
14	983.5	35.6	241	2	Q9CX88
15	930	33.7	193	2	Q8BWJ6
16	812.5	29.4	393	1	C1W4_HUMAN
17	790	28.6	398	1	C1W4_MOUSE
18	778	28.2	397	2	Q92414
19	512	18.6	309	1	C1WG_HUMAN
20	504	18.3	294	2	Q6X6Z5
21	483	17.5	499	1	C1W5_HUMAN
22	478.5	17.3	502	2	Q9TK62
23	477	17.3	448	2	Q6PFU3
24	460	16.7	262	2	Q6X6Z3
25	454	16.4	257	2	Q80XE0
26	452	16.4	322	2	Q6X6Z4
27	447	16.2	184	2	Q8N4V5
28	424.5	15.4	341	2	Q8H2T2
29	403	14.6	307	2	Q80IT4
30	400	14.6	336	1	C1W1_HUMAN
31	400	14.5	336	2	Q9Z2T2

32 398 14.4 336 2 Q8R454
33 395.5 14.3 336 2 Q99L99
34 392 14.2 332 1 C1WH_HUMAN
35 390.5 14.1 336 1 C1W1_MOUSE
36 382 13.8 259 2 Q02821
37 371.5 13.5 323 2 Q6PE11
38 360 13.0 331 2 Q8AV15
39 352.5 12.8 409 1 C1W3_MOUSE
40 352.5 12.8 411 1 C1W3_RAT
41 351.5 12.7 299 2 Q9QX34
42 350.5 12.7 365 1 C1W9_CAVPO
43 349.5 12.7 394 1 C1W3_HUMAN
44 349 12.6 396 2 Q9Z3V6
45 348.5 12.6 318 1 C1WF_RAT

ALIGNMENTS

RESULT 1

CIWA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q8TDK7; Q8TDK8; Q9HB59;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).
GN Name=KCNK10; Synonyms=TREK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20435789; PubMed=1080510; DOI=10.1074/jbc.M002822200;
RA Leage F., Terrenoire C., Romey G., Lazdunski M.;
RT "Human TREK2, a 2p domain mechano-sensitive K+ channel with multiple regulations by polyunsaturated fatty acids, lysophospholipids and Gs, Gi, and Gq protein-coupled receptors.";
RT J. Biol. Chem. 275:28398-28405 (2000).
RN [2]
SEQUENCE FROM N.A. (ISOFORMS B AND C).
RX MEDLINE=21895087; PubMed=11897838;
RA Gu W., Schlichtthorl G., Hirsch J.R., Engels H., Karschin C., Karschin A., Derst C., Steinlein O.K., Daut J.;
RT "Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain potassium channel TREK-2.";
RL J. Physiol. (Lond.) 539:657-668 (2002).
CC -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents. Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=A; Synonyms=TREK-2a;
CC IsoId=P57789-1; Sequence=Displayed;
CC Name=B; Synonyms=TREK-2b;
CC IsoId=P57789-2; Sequence=VSP_006697;
CC Name=C; Synonyms=TREK-2c;
CC IsoId=P57789-3; Sequence=VSP_006698;
CC -!- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney to a lower level in brain, testis, colon, and small intestine. Isoform b is strongly expressed in kidney (primarily in the proximal tubule) and pancreas, whereas isoform c is abundantly expressed in brain.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

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Best Local Similarity 94.3%; Pred. No. 9e-124;
Matches 433; Conservative 6; Mismatches 11; Indels 9; Gaps 3;

QY 1 MEPLTYDPL--SLVAVPAA--PVCPKSAATGQPPAPPTPTPLRSSSRATVVARMEG 57
DB 1 MYFSYIGYFFPLPLVAVPAAAPVCPKSAATG-----HPVPLRSSSRATVVARMEG 54

QY 58 TSQGGLOTVMKWTVAIFVWVVLVTGGLVFRALQPFSSQKNTIALEKAEFLRDHV 117
DB 55 ASQGGLOTVMKWTVAIFVWVVLVTGGLVFRALQPFSSQKNTIALEKAEFLRDHI 114

QY 118 CVSPQELFLIHALDADNAGVSPIGNSSSHDGLSAPFAGTPTITIGYNIAPST 177
DB 115 CVSPQELFLIHALDADNAGVSPIGNSSSHDGLSAPFAGTPTITIGYNIAPST 174

QY 178 EGKIFCILYALFGPLFGLAGIDGLGTIFGSIARVEKVKQVQSKIRVIST 237
DB 175 EGKIFCILYALFGPLFGLAGIDGLGTIFGSIARVEKVKQVQSKIRVIST 234

QY 238 LFLIAGCIVFVPIPAVIFKYIEGWTALSIYFVWVLTGFGDFVAGNAGINREWK 297
DB 235 LFLIAGCIVFVPIPAVIFKYIEGWTALSIYFVWVLTGFGDFVAGNAGINREWK 294

QY 298 PLVFWILVGLYFAVLSMIGDMLRVLSKTKVEVGEIKAHAAEWKANVTAEPRETRR 357
DB 295 PLVFWILVGLYFAVLSMIGDMLRVLSKTKVEVGEIKAHAAEWKANVTAEPRETRR 354

QY 358 LSVETHDKLORATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESIN 417
DB 355 LSVETHDKLORATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESIN 414

QY 418 NRPNNLRKGPQLNKHGQAGSEDNINKFGSTSLTKR 456
DB 415 NRPNNLRKGPQLNKHGQAGSEDNINKFGSTSLTKR 453

RESULT 7
Q68EY1 PRELIMINARY; PRT; 546 AA.

AC Q68EY1
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE LOC446288 protein (Fragment).
GN Name=LOC446288;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]

Q68EY1 TISSUE=Eye;
RC TISSUE=Eye;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]

SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC080069; AAH80069.1; --
DR InterPro: IPR003280; K-channel_2pore.
DR InterPro: IPR001622; K-channel_pore.
DR InterPro: IPR003976; Trek_channel.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01499; TREKCHANNEL.
FT NON TER 546
SQ SEQUENCE 546 AA; 60977 MW; AF6C7FB34AD34A06 CRC64;

Query Match 76.7%; Score 2117; DB 2; Length 546;
Best Local Similarity 78.8%; Pred. No. 7.8e-120;
Matches 419; Conservative 47; Mismatches 54; Indels 12; Gaps 5;

QY 13 VAVPAAAPVCP-----KSATNGQPPAPPTPTPLRSSSRATVVARMEGTSQGLQV 66
DB 18 VAVPAAVTPAPPPEPPSEPKNGHQHTTATPRMSVCSKSTLVSTMDNTS--SGLHSV 76

QY 67 MKWKTVAIFVWVVLVTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCSPOLEST 126
DB 77 MKWKTVAIFVWVVLVTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCSPOLEST 136

QY 127 LIQHALDADNAGVSPIGNSSSHDGLSAPFAGTPTITIGYNIAPSTEGKIFCIL 186
DB 137 LIKRAIDADNAGVSPIGNSSSHDGLSAPFAGTPTITIGYNIAPSTEGKIFCIL 196

QY 187 YAIFGIPLFGIAGIDGLGTIFGSIARVEKVKQVQSKIRVISTILFILAGCIV 246
DB 197 YAIFGIPLFGIAGIDGLGTIFGSIARVEKVKQVQSKIRVISTILFIVAGCIV 256

QY 247 FVTIPAVIFKYIEGWTALSIYFVWVLTGFGDFVAGNAGINREWKVPLVFWILV 306
DB 257 FVTIPAVIFKYIEGWTALSIYFVWVLTGFGDFVAGNAGINREWKVPLVFWILV 316

QY 307 GLAYFAAVLSMIGDMLRVLSKTKVEVGEIKAHAAEWKANVTAEPRETRRSLVEIHDKL 366
DB 317 GLAYFAAVLSMIGDMLRVLSKTKVEVGEIKAHAAEWKANVTAEPRETRRSLVEIHDKL 376

QY 367 QRAATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESINRPNRLRK 426
DB 377 QRAATIRSMERRRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSOESINRPNRLRK 436

QY 427 GPEQLNKHGQAGSEDNINKFGS--TSRLTKRKNKDKKTLPEDEVOKYKTFPNYSLDEEK 485
DB 437 EAEQTLHGQGVSEDNINKFGS--TSRLTKRKNKDKKTLPEDEVOKYKTFPNYSLDEEK 496

QY 486 KEEETKMCNSDNTSMTLTCIOQHALENGMIPTDKOREPENNSLLEDR 537
DB 497 KEDEDDTISTD---TATLSDFL-RHSIENGSIPTNETKEEESHESKALLEEK 544

RESULT 8

CIW2 MOUSE
ID CIW2 MOUSE STANDARD; PRT; 411 AA.
AC P97438;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium

DE channel protein TREK-1) (Two-pore potassium channel TPKC1) (TREK-1 K+ channel subunit).

GN Name=Kcnk2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=97157476; PubMed=9003761;

RA Pink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C., Lazdunski M.;

RT "Cloning, functional expression and brain localization of a novel unconventional outward rectifier K⁺ channel.";

RL EMBO J. 15:6854-6862(1996).

RN [2]

RP REVISIONS.

RC TISSUE=Brain;

RA Pink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C., Lazdunski M.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP ACTIVATION.

RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;

RA Patel A.J., Honore E., Lesage F., Pink M., Romey G., Lazdunski M.;

RT "Inhalational anesthetics activate two-pore-domain background K⁺ channels.";

RL Nat. Neurosci. 2:422-426(1999).

CC -!- FUNCTION: Outward rectifying potassium channel.

CC -!- SUBUNIT: Homodimer (Potential).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: High expression in brain and lung. Also detected in kidney, heart and skeletal muscle. Not detected in liver. In the brain, highest expression in olfactory bulb, hippocampus and cerebellum.

CC -!- MISCELLANEOUS: Inhibited by barium. Activated by volatile general anesthetics such as chloroform, diethyl ether, halothane and isoflurane.

CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

CC -----

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CC -----

DR EMBL; U73488; AAC53005.2; -

DR MGD; MGI:109366; Kcnk2.

DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.

DR GO; GO:0005249; P:voltage-gated potassium channel activity; IDA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IDA.

DR GO; GO:0006813; P:potassium ion transport; IDA.

DR InterPro; IPR003280; K+channel 2pore.

DR InterPro; IPR001622; K+channel pore.

DR InterPro; IPR003976; Trek channel.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01499; TREKCHANNEL.

DR Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transmembrane; Voltage-gated channel.

KW Potassium channel; Transmembrane; Transmembrane; Voltage-gated channel.

FT DOMAIN 1 46 Cytoplasmic (Potential).

FT TRANSMEM 67

FT DOMAIN 129 155 Pore-forming 1 (Potential).

FT TRANSMEM 157 177 Potential.

FT DOMAIN 178 207 Cytoplasmic (Potential).

FT TRANSMEM 208 228 Potential.

FT DOMAIN 238 268 Pore-forming 2 (Potential).

FT TRANSMEM 273 293 Potential.

FT DOMAIN 294 411 Cytoplasmic (Potential).

FT DOMAIN 378 411 Essential for chloroform and halothane

FT DOMAIN 354 411 sensitivity.

FT CARBOHYD 95 Required for basal channel activity.

FT CARBOHYD 119 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 411 AA; 45297 MW; 89976DDD103EPA05 CRC64;

Query Match 45.3%; Score 1251.5; DB 1; Length 411;

Best Local Similarity 64.3%; Pred. No. 1.2e-67;

Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCPKSNQPPAPAPPTPRLSISSRATVVA-RMEGTSOGGLQTKWKIVAI 75

Db AAPDLLDPKSA-----AQNKPRLSFSSKPTVLASRVESDS---AINVMKWTVTI 50

QY 76 FVVVVVLTGCLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQSLLETLIQHALDAD 135

Db FLVVVLYLIIGAAVFKALEQPEISQRTTIVIQKTFIAQHACVNSTELDELIIQIVAAI 110

QY 136 NAGVSPGNSNNSSHWDLGSAFFPAGTIVITIGVNTIAPSTEGGKIFCILYVAFGIPLF 195

Db NAGIPIGNSNQVSHWDLGSSFPFAGTIVITIGVNTIAPSTEGGKIFCIYVALLGIPLF 170

QY 196 GFLLAGIGDGLGTIFGKSIARVKKVQKVSQTKIRVISTILETLACIVPVTTPAVIF 255

Db GFLLAGVGDQLGTIFGKIAKVEDTFIKWVSQTKIRIITIIIFLPGCVLVALPAVIF 230

QY 256 KYIEGWTALSIYFVWVTLTTVGFDFVAGNAGINREWKPLVWFVILVGLAYFAAVL 315

Db KHIEGWSALDAIFYVWVTLTTVGFDFVAGNAGINREWKPLVWFVILVGLAYFAAVL 289

QY 316 SMIGDLRLVSKTKKEVEGEIKAAHAEKANTVAFETRRRLSVEIHDKLQRAATIRSM 375

Db SMIGDLRLVSKTKKEVEGEIPEHAAEANTVAFETRRRLSVEIHDKLQRAATIRSM 346

QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399

Db -KRKLSAELAGNHNOELTPCRRTL 369

RESULT 9

Q6P6P9 PRELIMINARY; PRT; 414 AA.

ID Q6P6P9

AC Q6P6P9, 27, Created

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Kcnk2 protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Carninci S.J., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

01-MAR-2003 (TREMBlrel. 23, Created)
 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Potassium channel subfamily K member 2.
 GN Name=Kcnk2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=22370953; PubMed=12368289; DOI=10.1074/jbc.M207233200;
 RA Enyeart J.J., Xu L., Danthi S., Enyeart J.A.;
 RT "An ACPH- and ATP-regulated background K⁺ channel in adrenocortical
 cells is TREK-1";
 RL J. Biol. Chem. 277:49186-49199(2002).
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 (TC 1.A.1.8) family.
 DR EMBL; AY148474; AAN37591.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; P:ion channel activity; IEA.
 DR GO; GO:0005267; P:potassium channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K-channel 2pore.
 DR InterPro; IPR001622; K-channel pore.
 DR InterPro; IPR003976; Trek channel.
 DR PRINTS; PR01333; 2PORECHANNEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 DR KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;
 Query Match 45.1%; Score 1244.5; DB 2; Length 411;
 Best Local Similarity 63.5%; Pred. No. 3.1e-67;
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
 QY 17 AAAPVCPKSNATNGQPPAPAPPTPTPLSLSSRATVVA-RMEGTSGGGLQTVWKKTVAI 75
 DB 2 AAPLLDPKSA-----AQNPKRLSFTKPTVLASRVSDT---TINWKKTVSTI 50
 QY 76 FVVVVVYLVGTGLVFRALAEQPFSSQKNTIALEKAEFLRDHVCVSPQBLETLIQHALDAD 135
 DB 51 FLVVVLYLIIGATVTKALEQPHIEISQRTTIVIQKTFISQACVNSTELDELIOQIVAAI 110
 QY 136 NAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTIGVGNAPSTEGGKIFCILYAFGIPLF 195
 DB 111 NAGIPLGNTSNQISHWDLGSSFPFAGTAVTTTIGVGNISPRTEGGKIFCIYALLGIPLF 170
 QY 196 GFLLAGIGDQGTIFGKSIARVEKVRKQVSKIRVISTILFTLAGCIVFVTPAVIF 255
 DB 171 GFLLAGVGDQGTIFGKGIARVEDTIFKNVSVQTKIRIISTITIFLFGCVLFVALPILF 230
 QY 256 KYIEGWTALSIYFVVTITLVGDFVAGGNAGINREWKPLVFWILVGLAYFAAVL 315
 DB 231 KHIEGWSALDAIFVVTITLVGDFVAGG-SDIEYLDFFKPVVFWILVGLAYFAAVL 289
 QY 316 SMIGDWLRLVSKTVEFGEIKAHAEKANKVTAFTTRRLSVEIHDKIQRAATIRSM 375
 DB 290 SMIGDWLRLVSKTVEFGEFRAHAETANTVTAFTTRRLSVEIYDKFQRTSI--- 346
 QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
 DB 347 -KRKLASBLAGNHQELTPCRNL 369
 RESULT 12
 Q9NRT2 PRELIMINARY; PRT; 411 AA.
 AC Q9NRT2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily
 K, member 2).
 GN Name=TREK-1; Synonyms=KCNK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20244931; PubMed=10784345;
 RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
 RA Medhurst A.D., Murdock P., Chapman C.G.;
 RT "Cloning, localisation and functional expression of the human
 orthologue of the TREK-1 potassium channel";
 RL Pflugers Arch. 439:714-722(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smaltus D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 (TC 1.A.1.8) family.
 DR EMBL; AF171068; AAF89743.1; -;
 DR EMBL; BC069462; AAH69462.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; P:ion channel activity; IEA.
 DR GO; GO:0005267; P:potassium channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K-channel 2pore.
 DR InterPro; IPR001622; K-channel pore.
 DR InterPro; IPR003976; Trek channel.
 DR PRINTS; PR01333; 2PORECHANNEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 DR KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45494 MW; PDE40CAB21B42A1C CRC64;
 Query Match 45.0%; Score 1242.5; DB 2; Length 411;
 Best Local Similarity 63.5%; Pred. No. 4.1e-67;
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
 QY 17 AAAPVCPKSNATNGQPPAPAPPTPTPLSLSSRATVVA-RMEGTSGGGLQTVWKKTVAI 75
 DB 2 AAPLLDPKSA-----AQNPKRLSFTKPTVLASRVSDT---TINWKKTVSTI 50
 QY 76 FVVVVVYLVGTGLVFRALAEQPFSSQKNTIALEKAEFLRDHVCVSPQBLETLIQHALDAD 135
 DB 51 FLVVVLYLIIGATVTKALEQPHIEISQRTTIVIQKTFISQACVNSTELDELIOQIVAAI 110
 QY 136 NAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTIGVGNAPSTEGGKIFCILYAFGIPLF 195
 DB 111 NAGIPLGNTSNQISHWDLGSSFPFAGTAVTTTIGVGNISPRTEGGKIFCIYALLGIPLF 170
 QY 196 GFLLAGIGDQGTIFGKSIARVEKVRKQVSKIRVISTILFTLAGCIVFVTPAVIF 255
 DB 171 GFLLAGVGDQGTIFGKGIARVEDTIFKNVSVQTKIRIISTITIFLFGCVLFVALPILF 230
 QY 256 KYIEGWTALSIYFVVTITLVGDFVAGGNAGINREWKPLVFWILVGLAYFAAVL 315
 DB 231 KHIEGWSALDAIFVVTITLVGDFVAGG-SDIEYLDFFKPVVFWILVGLAYFAAVL 289
 QY 316 SMIGDWLRLVSKTVEFGEIKAHAEKANKVTAFTTRRLSVEIHDKIQRAATIRSM 375
 DB 290 SMIGDWLRLVSKTVEFGEFRAHAETANTVTAFTTRRLSVEIYDKFQRTSI--- 346
 QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
 DB 347 -KRKLASBLAGNHQELTPCRNL 369

Db 51 FLVVLVLIIGATVFKALQEPHEISQRTTIVIQKTFISQHSVCVNSTELDELIQIIVAAI 110
 Qy 136 NAGVSPIGNSSNHHWDGSAFFAGTIVITIGVNIAPSTEGGKIFCIIYVAFGIPUF 195
 Db 111 NAGIPLGNTSNQISHWDGSGFFAGTIVITIGFNGISPRTEGGKIFCIIYVAFGIPUF 170
 Qy 196 GFLLAGIGDQGTIFGKSARVEKVRKQVSTQIRVISTITLFLAGCIVFTTIPAVIF 255
 Db 171 GFLLAGVGDQGTIFGKIAKVEDTFIKWVSQTKIRIISTITLFLGCVLFPALP 230
 Qy 256 KYIEGWTALESIFVVTTLTGVGDFVAGNAGINREWYKPLVWFWLVLGLAYFAVL 315
 Db 231 KHIEGWSALDAIFVVTITLTGFGDYVAGG-SDIEYLDYFVWVFWLVLGLAYFAVL 289
 Qy 316 SMIGDLRLVLSKTKKEVEGEIKAHAAEWKANTVAFPRTRRLSVEIHDKLOAATIRSM 375
 Db 290 SMIGDLRLVLSKTKKEVEGEFRAHAAEWNTVAFPRTRRLSVEIHDKLOAATIRSM 346
 Qy 376 ERRRLGLDQRAHSLDMLSPKRSV 399
 Db 347 -KRKLSAELAGNHQELTFCRRTL 369

RESULT 13

CIW2 HUMAN
 AC Q95069; O9UNE3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (two-pore potassium channel TPCK1).
 GN Name=CKNK2; Synonyms=TREK, TREK1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+ channels";
 RL Nat. Neurosci. 2:422-426(1999).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Outward rectifying potassium channel.
 CC -!- SUBUNIT: Homodimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- MISCELLANEOUS: Activated by volatile general anaesthetics such as chloroform, halothane and isoflurane.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF129399; RAD47569.1; -
 CC EMBL; AF004711; RAD01203.1; -
 CC Genew; HGNC:6277; KCNK2.
 CC MIM; 603219;
 CC GO; GO:0016020; C:membrane; NAS.
 CC GO; GO:0015271; P:outward rectifier potassium channel activity; NAS.
 CC GO; GO:0006813; P:potassium ion transport; NAS.

DR InterPro; IPR003280; K+channel 2pore.
 DR InterPro; IPR001622; K+channel pore.
 DR InterPro; IPR003976; Trek channel.
 DR PRINTS; PR01333; 2POREKCHANEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 KW Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.
 FT DOMAIN 1 61
 FT TRANSMEM 62 82
 FT DOMAIN 144 170
 FT TRANSMEM 172 192
 FT DOMAIN 193 223
 FT TRANSMEM 224 244
 FT DOMAIN 253 283
 FT TRANSMEM 288 308
 FT DOMAIN 309 426
 FT TRANSMEM 378 426
 FT DOMAIN 354 426
 FT CARBOHYD 110 110
 FT CARBOHYD 134 134
 FT CONFLICT 2 16
 FT CONFLICT 309 311
 FT CONFLICT 391 391
 FT CONFLICT 411 411
 SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;
 Query Match 44.1%; Score 1218.5; DB 1; Length 426;
 Best Local Similarity 62.8%; Pred. NO. 1.2e-65;
 Matches 241; Conservative 58; Mismatches 68; Indels 17; Gaps 5;
 Qy 17 AAAPVCPQPSKATNGPPAPPTPTPLSLSSRATVVA-RMEGTSQGLQTVNKKTKVVAI 75
 Db 17 AAPLLDPKSA-----AONKRLSFSTKPTVLASRVSDT---TINVMKTVSTI 65
 Qy 76 FVVVVVLTGVLVFRALQEPSSQKNTIALEKAEPLRDHVCSPQELTILQIHALDAD 135
 Db 66 FLVVLVLIIGATVFKALQEPHEISQRTTIVIQKTFISQHSVCVNSTELDELIQIIVAAI 125
 Qy 136 NAGVSPIGNSSNHHWDGSAFFAGTIVITIGVNIAPSTEGGKIFCIIYVAFGIPUF 195
 Db 136 NAGIPLGNTSNQISHWDGSGFFAGTIVITIGFNGISPRTEGGKIFCIIYVAFGIPUF 185
 Qy 196 GFLLAGIGDQGTIFGKSARVEKVRKQVSTQIRVISTITLFLAGCIVFTTIPAVIF 255
 Db 186 GFLLAGVGDQGTIFGKIAKVEDTFIKWVSQTKIRIISTITLFLGCVLFPALP 245
 Qy 256 KYIEGWTALESIFVVTTLTGVGDFVAGNAGINREWYKPLVWFWLVLGLAYFAVL 315
 Db 246 KHIEGWSALDAIFVVTITLTGFGDYVAGG-SDIEYLDYFVWVFWLVLGLAYFAVL 304
 Qy 316 SMIGDLRLVLSKTKKEVEGEIKAHAAEWKANTVAFPRTRRLSVEIHDKLOAATIRSM 375
 Db 305 SMIGDLRLVLSKTKKEVEGEFRAHAAEWNTVAFPRTRRLSVEIHDKLOAATIRSM 361
 Qy 376 ERRRLGLDQRAHSLDMLSPKRSV 399
 Db 362 -KRKLSAELAGNHQELTFCRRTL 384
 RESULT 14
 Q9CX88
 ID Q9CX88 PRELIMINARY; PRT; 241 AA.
 AC Q9CX88;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:301005K24 product:POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog.
 GN Name=170002423Rik;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RA The RIKEN Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura K., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK019376; BAB1686.1;
 DR MG; MG1:1919508; 1700024D3R1k.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005216; P:ion channel activity; IEA.
 DR GO; GO:0005267; P:potassium channel activity; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR009056; Cytochrome c.
 DR InterPro; IPR001622; K-channel pore.
 DR InterPro; IPR003976; Trek_channel.

DR PRINTS; PR01499; TREKCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 241 AA; 25799 MW; B4C39F77CD0A39DA CRC64;
 Query Match 35.6%; Score 983.5; DB 2; Length 241;
 Best Local Similarity 93.4%; Pred. NO. 9.8e-52;
 Matches 197; Conservative 3; Mismatches 4; Indels 7; Gaps 2;
 QY 13 VAVPAAA-PVCQPKSATNGQPAPAPTPTPLRLSISRRATVVARMEGTSGGGLQTVNKKWT 71
 DB 18 VAVPAAAAPPVCQPKSATNGH-----HPVPLRLSISRRATVVARMEGASGGGLQTVNKKWT 71
 QY 72 VVAIFVVVVVYLVTVGLVFRALQPFSSQKNTALEKAEFLRDHVCVSPQLETLIQHA 131
 DB 72 VVAIFVVVVVYLVTVGLVFRALQPFSSQKNTALEKAEFLRDHVCVSPQLETLIQHA 131
 QY 132 LDADNAGVSPGNSNNSHWDLGSAFPFAGTIVTTIGYNIAPSTEGGKIFCILYAIFG 191
 DB 132 LDADNAGVSPGNSNNSHWDLGSAFPFAGTIVTTIGYNIAPSTEGGKIFCILYAIFG 191
 QY 192 IPLFGFLLAGIGDQDGLTIFGKSIARVEKVF 222
 DB 192 IPLFGFLLAGIGDQDGLTIFGKSIARVEKVF 222
 RESULT 15
 Q8BWJ6 PRELIMINARY; PRT; 193 AA.
 ID Q8BWJ6
 AC Q8BWJ6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched
 DE library, clone: p330028p16 product: POTASSIUM CHANNEL SUBFAMILY K MEMBER
 DE 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+
 DE CHANNEL SUBUNIT) homolog (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RA The RIKEN Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=1107661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK052327; BAC34939.1; -
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON TER
SQ SEQUENCE 193 AA; 22174 MW; 8CCBADA59BF60641 CRC64;
Query Match 33.7%; Score 930; DB 2; Length 193;
Best Local Similarity 93.8%; Pred. NO. 1.3e-48;
Matches 181; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 346 NVTAFRETRRLSVEIHDKLRATIRSMERRRLGLDQRAHSLDMLSPKESVFAALDT 405
DB 1 NVTAFREARRRLSVEIHDKLRATIRSMERRRLGLDQRAHSLDMLSPKESVFAALDT 60
QY 406 GRFKASSQESINRRPNLRLKGPQLNKGQASDNIINFGSTSLTKRNKDLKCTL 465
DB 61 GRFKASSQESINRRPNLRLKGPQLTKHGQASDNIINFGSTSLTKRNKDLKCTL 120
QY 466 PEDVQIKYKTFRNYSIDEEKKEETKMCNDSNTAMLTDCIQQAELNGMIPTDTKD 525
DB 121 PEDVQIKYKTFRNYSIDEEKKEETKMCNDSNTAMLTDCIQQAELNGMWVPTDTKD 180
QY 526 REPENNSLLEDRN 538
DB 181 QGLENNLSLEDRN 193
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